

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 25, 2002, 09:49:41 : Search time 32.67 Seconds
(without alignments)
1115.158 Million cell updates/sec

Title: US-09-184-826-2

Perfect score: 328
Sequence: 1 MMDLRLLILIVGAIIIAL.....TPQKREYQDIIRKVDANA 328

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_032802.*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	328	100.0	328	19	AAW36984
2	227	69.2	328	22	AAW65926
3	182	55.5	864	22	ABG21781
4	117	35.7	144	22	AAW65925
5	21	6.4	328	22	AAW65927
6	11	3.4	328	22	AAW65928
7	9	2.7	322	20	AAW81571
8	9	2.4	36	22	AAW81570
9	8	2.4	41	22	AAO03175
10	8	2.4	41	22	AAW87430
11	8	2.4	42	22	AAO13330

12	8	2.4	44	22	AAO13438	Human polypeptide
13	8	2.4	45	22	ABG05119	Novel human diapo
14	8	2.4	45	22	AAO13238	Human polypeptide
15	8	2.4	46	22	AAO02012	Human polypeptide
16	8	2.4	46	22	AAO13301	Human polypeptide
17	8	2.4	46	22	AAO13371	Human polypeptide
18	8	2.4	47	22	AAO13321	Human polypeptide
19	8	2.4	48	22	AAO12235	Human polypeptide
20	8	2.4	48	22	AAO13324	Human polypeptide
21	8	2.4	49	22	AAW82671	Human polypeptide
22	8	2.4	51	22	AAO13292	Human polypeptide
23	8	2.4	52	22	AAO11267	Human polypeptide
24	8	2.4	53	22	AAO02933	Human polypeptide
25	8	2.4	53	22	AAO07312	Human polypeptide
26	8	2.4	55	22	AAO11261	Human polypeptide
27	8	2.4	56	22	AAW83482	Human polypeptide
28	8	2.4	57	22	AAU32261	Novel human secret
29	8	2.4	57	22	AAO02004	Human polypeptide
30	8	2.4	58	22	AAO00928	Human polypeptide
31	8	2.4	58	22	AAO09102	Human polypeptide
32	8	2.4	59	22	AAW82906	Human polypeptide
33	8	2.4	59	22	AAW91350	Human polypeptide
34	8	2.4	59	22	AAO11369	Human polypeptide
35	8	2.4	60	22	AAO08264	Human polypeptide
36	8	2.4	60	22	AAO12892	Human polypeptide
37	8	2.4	61	22	AAU29820	Novel human secret
38	8	2.4	61	22	AAW88413	Human polypeptide
39	8	2.4	62	22	AAU31244	Novel human secret
40	8	2.4	65	22	AAO10147	Human polypeptide
41	8	2.4	70	22	AAU57572	Protonibacterium
42	8	2.4	71	22	AAW84721	Human polypeptide
43	8	2.4	75	22	AAO10281	Human polypeptide
44	8	2.4	77	22	AAW82766	Human polypeptide
45	8	2.4	78	22	AAW87504	Human polypeptide
46	8	2.4	79	22	AAW89885	Human polypeptide
47	8	2.4	86	22	AAW78222	Human polypeptide
48	8	2.4	102	22	AAO00087	Human polypeptide
49	8	2.4	107	22	AAW83240	Human polypeptide
50	8	2.4	104	22	AAW82823	Human polypeptide
51	8	2.4	108	22	AAU29906	Novel human secret
52	8	2.4	110	22	AAO10290	Human polypeptide
53	8	2.4	116	22	AAO11339	Human polypeptide
54	8	2.4	133	22	AAO09775	Human polypeptide
55	8	2.4	204	22	AAW93105	Human polypeptide
56	8	2.4	441	21	AAW95324	Xenopus neurogen
57	8	2.4	620	22	ABW69388	Drosophila melanog
58	8	2.4	635	22	ABG24694	Novel human diapo
59	8	2.4	1476	22	ABW58706	Drosophila melanog
60	8	2.4	2485	21	AAW18172	Plasmodium falcipa
61	7	2.1	17	21	AAW56605	Human prostate can
62	7	2.1	30	22	AAO05096	Human polypeptide
63	7	2.1	32	22	AAO13313	Human polypeptide
64	7	2.1	36	22	AAO08134	Human polypeptide
65	7	2.1	39	22	AAO02750	Human polypeptide
66	7	2.1	41	22	AAO13305	Human polypeptide
67	7	2.1	41	22	AAO13380	Human polypeptide
68	7	2.1	42	22	AAO08190	Human polypeptide
69	7	2.1	42	22	AAO13139	Human polypeptide
70	7	2.1	44	22	ABG05898	Novel human diapo
71	7	2.1	44	22	AAO09036	Human polypeptide
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73	7	2.1	45	22	AAO07898	Human polypeptide
74	7	2.1	47	22	AAO13250	Human polypeptide
75	7	2.1	48	22	ABW14527	Human polypeptide
76	7	2.1	48	22	AAU31261	Novel human secret
77	7	2.1	49	22	AAW87816	Human polypeptide
78	7	2.1	49	22	AAO10872	Human polypeptide
79	7	2.1	51	22	AAW82946	Human polypeptide
80	7	2.1	51	22	AAO11191	Human polypeptide
81	7	2.1	54	22	AAU31417	Novel human secret
82	7	2.1	59	22	AAO11590	Human polypeptide
83	7	2.1	61	22	AAW82759	Human polypeptide
84	7	2.1	61	22	AAO13159	Human polypeptide

85	7	2.1	63	22	AAU31255	Novel human secret	158	7	2.1	503	12	AAU14768	Metastasis-specific
86	7	2.1	63	22	AAU89389	Human immune/haema	159	7	2.1	571	21	AAU18914	A novel polypeptid
87	7	2.1	64	22	AAU31291	Novel human secret	160	7	2.1	571	21	AAU71107	Human Hydrilase pr
88	7	2.1	66	22	AAU08161	Human polypeptide	161	7	2.1	571	22	AAU12442	Human PRO1887 poly
89	7	2.1	67	22	AAU91338	Human immune/haema	162	7	2.1	571	22	AAU12442	Human gene 2 encod
90	7	2.1	68	22	ABU10869	Human ovarian and/	163	7	2.1	634	22	AAU04101	Novel human diagn
91	7	2.1	68	22	AAU95688	Human reproductive	164	7	2.1	636	22	AAU06059	C. elegans UNC-5 p
92	7	2.1	68	22	AAU91606	Human immune/haema	165	7	2.1	683	22	AAU06059	C. elegans UNC-5 p
93	7	2.1	70	22	AAU05962	Human polypeptide	166	7	2.1	688	21	AAU57898	Human transmembran
94	7	2.1	80	22	AAU31245	Novel human secret	167	7	2.1	696	22	AAU57898	Drosophila melanog
95	7	2.1	81	22	ABU70451	Drosophila melanog	168	7	2.1	717	22	AAU31581	Amilo acid sequenc
96	7	2.1	81	22	AAU31246	Novel human secret	169	7	2.1	818	22	AAU322737	C. glutaminc prote
97	7	2.1	81	22	AAU85296	Human immune/haema	170	7	2.1	856	21	AAU27656	Human protein PRO3
98	7	2.1	81	22	AAU11456	Human polypeptide	171	7	2.1	1006	19	AAU70525	Human thymus recep
99	7	2.1	82	22	ABU17455	Human nervous syst	172	7	2.1	1006	19	AAU722296	Human receptor typ
100	7	2.1	82	22	AAU03440	Human polypeptide	173	7	2.1	1021	19	AAU70526	Human thymus recep
101	7	2.1	82	22	AAU09921	Human polypeptide	174	7	2.1	1049	22	ABU71939	Drosophila melanog
102	7	2.1	85	22	AAU82715	Human immune/haema	175	7	2.1	1123	22	ABU59522	Drosophila melanog
103	7	2.1	86	22	ABU16536	Human nervous syst	176	7	2.1	1144	22	AAU50658	C. elegans UNC-5 p
104	7	2.1	87	21	AAU02575	Human secreted pro	177	7	2.1	1191	22	ABU12436	Novel human diagn
105	7	2.1	92	22	AAU09773	Human polypeptide	178	7	2.1	1233	22	ABU69686	Drosophila melanog
106	7	2.1	96	22	AAU10039	Human polypeptide	179	7	2.1	1274	22	ABU69686	Drosophila melanog
107	7	2.1	100	22	AAU12825	Human polypeptide	180	7	2.1	2977	22	ABU69480	Drosophila melanog
108	7	2.1	108	22	AAU11505	Human polypeptide	181	7	2.1	2977	22	ABU69480	Drosophila melanog
109	7	2.1	112	21	AAU55843	P. ciferiti serine	182	7	2.1	5533	22	ABU65772	Drosophila melanog
110	7	2.1	113	22	AAU83410	Human immune/haema	183	7	2.1	5560	22	ABU71160	Drosophila melanog
111	7	2.1	118	22	ABU23223	Novel human diagn	184	6	1.8	10	16	AAU08806	YES protein tyrosi
112	7	2.1	120	22	AAU29870	Novel human secret	185	6	1.8	11	22	AAU25805	Breast cancer cell
113	7	2.1	128	21	AAU33256	Zea mays protein f	186	6	1.8	12	21	AAU18815	Immunogenic peptid
114	7	2.1	131	21	AAU01801	Human secreted pro	187	6	1.8	13	22	AAU98136	Human peptide #141
115	7	2.1	142	22	AAU24261	Human EST encoded	188	6	1.8	14	21	AAU51020	Pollu virus B deri
116	7	2.1	144	21	AAU18062	Arabidopsis thalia	189	6	1.8	20	21	AAU33936	Human secreted pro
117	7	2.1	148	18	AAU31605	Calcitonin gene re	190	6	1.8	20	21	AAU53681	Peptide sequence 1
118	7	2.1	149	21	AAU18061	Arabidopsis thalia	191	6	1.8	20	21	AAU53684	Peptide sequence 1
119	7	2.1	157	22	AAU38747	Human polypeptide	192	6	1.8	20	21	AAU53685	Peptide 134-153: E1
120	7	2.1	160	22	AAU40533	Human polypeptide	193	6	1.8	20	22	AAU01826	Gamma gliadin T-ce
121	7	2.1	170	21	AAU41297	Arabidopsis thalia	194	6	1.8	20	22	AAU01426	Peptide #12 derlve
122	7	2.1	170	22	ABU17244	Human GTP-binding	195	6	1.8	23	10	AAU90452	Epitope recognized
123	7	2.1	199	22	ABU68517	Chlamydia trachoma	196	6	1.8	24	17	AAU87649	Synthetic Bordetel
124	7	2.1	222	20	AAU37757	Drosophila melanog	197	6	1.8	27	22	AAU01471	Human polypeptide
125	7	2.1	223	22	ABU68114	Arabidopsis thalia	198	6	1.8	30	21	AAU45157	Human secreted pro
126	7	2.1	245	21	AAU37622	Arabidopsis thalia	199	6	1.8	31	12	AAU11737	Peptide 683 derlve
127	7	2.1	245	21	AAU39197	Arabidopsis thalia	200	6	1.8	31	12	AAU11739	Peptide BB05 derlve
128	7	2.1	246	20	AAU19840	B. burgdorferi ant	201	6	1.8	32	22	ABU38903	Peptide #6409 enco
129	7	2.1	251	21	AAU25671	Human secreted pro	202	6	1.8	32	22	ABU23896	Protein #5895 enco
130	7	2.1	252	22	AAU93763	Human protein sequ	203	6	1.8	32	22	AAU59554	Human brain expres
131	7	2.1	267	19	AAU81726	M. tuberculosis im	204	6	1.8	32	22	AAU72123	Human bone marrow
132	7	2.1	267	19	AAU64359	Mycobacterium tube	205	6	1.8	32	22	AAU19447	Peptide #7929 enco
133	7	2.1	267	20	AAU39156	M. tuberculosis an	206	6	1.8	32	22	AAU32385	Peptide #5881 enco
134	7	2.1	274	21	AAU39013	M. tuberculosis re	207	6	1.8	33	22	AAU40232	Peptide #6422 enco
135	7	2.1	274	21	AAU39196	Arabidopsis thalia	208	6	1.8	33	22	AAU61011	Peptide #7738 enco
136	7	2.1	281	22	AAU68133	Human AFP protein	209	6	1.8	33	22	AAU73706	Human brain expres
137	7	2.1	289	22	AAU65930	P. aeruginosa zipa	210	6	1.8	33	22	AAU33892	Human bone marrow
138	7	2.1	301	22	AAU90500	C. glutamicum prote	211	6	1.8	34	21	AAU35632	Peptide #7929 enco
139	7	2.1	318	22	AAU64426	Proionibacterium	212	6	1.8	34	22	AAU40280	Human secreted pro
140	7	2.1	335	21	AAU99350	Human PRO1378 (UNQ	213	6	1.8	34	22	AAU61073	Peptide #7786 enco
141	7	2.1	335	22	AAU29110	Human PRO polypept	214	6	1.8	34	22	AAU73776	Human brain expres
142	7	2.1	335	22	AAU66099	Protein of the inv	215	6	1.8	34	22	AAU33963	Peptide #8000 enco
143	7	2.1	342	22	AAU55616	Proionibacterium	216	6	1.8	38	21	AAU33781	Human secreted pro
144	7	2.1	344	22	AAU65929	S. putri zipa prot	217	6	1.8	38	22	AAU00823	Human polypeptide
145	7	2.1	356	17	AAU03136	Herpesvirus of tur	218	6	1.8	39	21	AAU34645	Gene 13 human secr
146	7	2.1	361	22	AAU03323	Herpesvirus of tur	219	6	1.8	39	22	AAU22337	Human cardiovascular
147	7	2.1	361	22	AAU68291	Drosophila melanog	220	6	1.8	39	22	AAU07416	Human polypeptide
148	7	2.1	366	22	AAU79122	Human protein seq	221	6	1.8	40	18	AAU10968	Human polypeptide
149	7	2.1	382	22	AAU80106	Human protein seq	222	6	1.8	40	22	AAU11155	Human polypeptide
150	7	2.1	392	22	AAU04176	Human gene 2 encod	223	6	1.8	41	21	AAU55544	Human prostate can
151	7	2.1	401	20	AAU17219	Human secreted pro	224	6	1.8	41	22	AAU40647	Peptide #8153 enco
152	7	2.1	401	22	AAU38989	Human secreted pro	225	6	1.8	41	22	AAU24904	Protein #6903 enco
153	7	2.1	401	22	AAU93152	Human protein sequ	226	6	1.8	41	22	AAU61507	Human brain expres
154	7	2.1	404	22	AAU82055	S. epidermidis ope	227	6	1.8	41	22	AAU74296	Human bone marrow
155	7	2.1	414	22	AAU04125	Human gene 2 encod	228	6	1.8	41	22	AAU20261	Peptide #6695 enco
156	7	2.1	427	19	AAU29661	Homo sapiens CT542	229	6	1.8	41	22	AAU34408	Peptide #8445 enco
157	7	2.1	467	22	ABU29595	Novel human diagn	230	6	1.8	42	16	AAU65288	Beta amyloid pepti

231	6	1.8	42	22	AAO13326	Human polypeptide	304	6	1.8	70	22	AAW82316	Human immune/haema
232	6	1.8	43	22	AAO07301	Human polypeptide	305	6	1.8	70	22	AAW19662	Peptide #6096 enco
233	6	1.8	43	22	AAW62252	Human secreted pro	306	6	1.8	70	22	AAW32877	Peptide #6914 enco
234	6	1.8	44	21	AAW29911	Human secreted pro	307	6	1.8	71	22	AAU44863	Propionibacterium
235	6	1.8	44	21	AAW34112	Human secreted pro	308	6	1.8	72	22	AAU63849	Propionibacterium
236	6	1.8	44	22	AAO12434	Human polypeptide	309	6	1.8	73	19	AAW60154	M. vaccae antigen
237	6	1.8	46	21	AAW34955	Gene 29 human secr	310	6	1.8	73	20	AAV14501	Nov. vaccae antigen
238	6	1.8	46	22	AAW30804	Peptide #3455 enco	311	6	1.8	73	22	AAW25287	Novel human diagno
239	6	1.8	46	22	AAW35981	Peptide #3487 enco	312	6	1.8	73	22	AAW34653	Peptide #11159 enc
240	6	1.8	46	22	AAW21391	Protein #3390 enco	313	6	1.8	73	22	AAW26604	Protein #8603 enco
241	6	1.8	46	22	AAW56783	Human brain expres	314	6	1.8	73	22	AAW64601	Human brain expres
242	6	1.8	46	22	AAW69161	Human bone marrow	315	6	1.8	73	22	AAW77392	Human bone marrow
243	6	1.8	46	22	AAW16992	Peptide #3426 enco	316	6	1.8	73	22	AAW21320	Peptide #7754 enco
244	6	1.8	46	22	AAW29484	Peptide #3521 enco	317	6	1.8	73	22	AAW37547	Peptide #11584 enc
245	6	1.8	46	22	AAW04699	Peptide #3381 enco	318	6	1.8	74	21	AAW01095	Human secreted pro
246	6	1.8	48	22	AAW87831	Human immune/haema	319	6	1.8	74	21	AAW01404	Human secreted pro
247	6	1.8	48	22	AAO13308	Human polypeptide	320	6	1.8	74	22	AAW89738	Human immune/haema
248	6	1.8	48	22	AAO13267	Human polypeptide	321	6	1.8	76	22	AAW91081	Human immune/haema
249	6	1.8	49	22	AAW89153	Human immune/haema	322	6	1.8	77	22	AAW50172	Propionibacterium
250	6	1.8	49	22	AAO10780	Human polypeptide	323	6	1.8	78	19	AAW73149	Bovine amphiregulin
251	6	1.8	50	22	AAW92465	C glutamicum prote	324	6	1.8	78	22	AAW91295	Human immune/haema
252	6	1.8	50	22	AAW62178	Human gene 23-enco	325	6	1.8	78	22	AAO11230	Human polypeptide
253	6	1.8	51	22	AAW56825	Propionibacterium	326	6	1.8	79	20	AAW22526	Yeast PABP#3 prote
254	6	1.8	51	22	AAW31465	Peptide #4116 enco	327	6	1.8	79	22	AAU47704	Propionibacterium
255	6	1.8	51	22	AAW36675	Peptide #4181 enco	328	6	1.8	79	22	AAW11661	Human secreted pro
256	6	1.8	51	22	AAW22011	Protein #4010 enco	329	6	1.8	80	21	AAW58222	Arbidopsia thalia
257	6	1.8	51	22	AAW54816	Human brain expres	330	6	1.8	80	22	AAW52512	Propionibacterium
258	6	1.8	51	22	AAW57438	Human brain expres	331	6	1.8	80	22	AAO07549	Human polypeptide
259	6	1.8	51	22	AAW69835	Human bone marrow	332	6	1.8	81	22	AAO07707	Human polypeptide
260	6	1.8	51	22	AAW17658	Peptide #4092 enco	333	6	1.8	82	10	AAW95451	Protein sequence e
261	6	1.8	51	22	AAW30176	Peptide #4213 enco	334	6	1.8	82	19	AAW73153	Human amphiregulin
262	6	1.8	51	22	AAW05318	Peptide #4000 enco	335	6	1.8	82	19	AAW73154	Human amphiregulin
263	6	1.8	52	22	AAW50961	Propionibacterium	336	6	1.8	83	17	AAW95150	Collagen like prot
264	6	1.8	53	22	AAW64820	Human secreted pro	337	6	1.8	83	22	AAW872775	Repetitive protein
265	6	1.8	53	22	AAW37886	AGRP-1 protein. S	338	6	1.8	83	22	AAW64045	CLP/CB-F-L2 functi
266	6	1.8	54	22	AAW38795	Peptide #6301 enco	339	6	1.8	84	10	AAW90449	Sequence of mature
267	6	1.8	54	22	AAW23827	Protein #5826 enco	340	6	1.8	85	21	AAW55714	Arbidopsia thalia
268	6	1.8	54	22	AAW59434	Human brain expres	341	6	1.8	85	21	AAW55923	Arbidopsia thalia
269	6	1.8	54	22	AAW71994	Human bone marrow	342	6	1.8	85	21	AAW60730	Arbidopsia thalia
270	6	1.8	54	22	AAW19397	Peptide #5831 enco	343	6	1.8	86	21	AAW01818	Human secreted pro
271	6	1.8	54	22	AAW32267	Peptide #6304 enco	344	6	1.8	88	22	AAW23394	Novel human diagno
272	6	1.8	55	22	AAW56731	Propionibacterium	345	6	1.8	88	22	AAU20670	Human novel foetal
273	6	1.8	55	22	AAW82725	Human immune/haema	346	6	1.8	88	22	AAW90638	Human immune/haema
274	6	1.8	57	21	AAW12378	Zea mays protein f	347	6	1.8	88	22	AAO10865	Human polypeptide
275	6	1.8	57	22	AAW70588	Drosophila melanog	348	6	1.8	89	21	AAW40881	Human ORFX ORF645
276	6	1.8	58	22	AAW25753	Human secreted pro	349	6	1.8	90	22	AAU43517	Propionibacterium
277	6	1.8	58	22	AAW67404	Propionibacterium	350	6	1.8	90	22	AAW63100	Propionibacterium
278	6	1.8	59	16	AAW73922	B. catarrhalis CD e	351	6	1.8	91	18	AAW37304	Amphiregulin AR97-
279	6	1.8	59	21	AAW33893	Human secreted pro	352	6	1.8	91	21	AAW34427	Arbidopsia thalia
280	6	1.8	59	22	AAW11231	Novel human diagno	353	6	1.8	96	22	AAW25845	Novel human diagno
281	6	1.8	60	22	AAW59902	Propionibacterium	354	6	1.8	96	22	AAW27873	Human peptide #524
282	6	1.8	60	22	AAW03492	Human musculoskele	355	6	1.8	96	22	AAW33044	Peptide #550 enco
283	6	1.8	60	22	AAO10971	Human polypeptide	356	6	1.8	96	22	AAW66229	Human bone marrow
284	6	1.8	62	21	AAW39027	Human secreted pro	357	6	1.8	96	22	AAW14099	Peptide #533 enco
285	6	1.8	62	22	AAW19857	Novel human diagno	358	6	1.8	96	22	AAW26506	Peptide #519 enco
286	6	1.8	63	22	AAW20392	Novel human diagno	359	6	1.8	96	22	AAW01837	Peptide #519 enco
287	6	1.8	63	22	AAW26590	Novel human diagno	360	6	1.8	98	22	AAU22330	Human cardiovascu
288	6	1.8	63	22	AAW05256	Mouse Nope (neighb	361	6	1.8	100	21	AAW10994	Zea mays protein f
289	6	1.8	64	22	AAW58572	Propionibacterium	362	6	1.8	100	21	AAW40677	Zea mays protein f
290	6	1.8	64	22	AAW14055	Novel human diagno	363	6	1.8	100	22	AAW05262	Novel human diagno
291	6	1.8	65	21	AAW02511	Human secreted pro	364	6	1.8	101	19	AAW20792	Human neurofilamen
292	6	1.8	65	22	AAW87348	Human immune/haema	365	6	1.8	101	22	AAW88555	Human immune/haema
293	6	1.8	67	21	AAW56331	Human secreted pro	366	6	1.8	102	21	AAW37517	Arbidopsia thalia
294	6	1.8	67	22	AAU23420	Novel human enzyme	367	6	1.8	103	21	AAW55713	Arbidopsia thalia
295	6	1.8	67	22	AAU16955	Human novel secret	368	6	1.8	104	21	AAW11664	A. vitis hypersens
296	6	1.8	68	22	AAW05266	Novel human diagno	369	6	1.8	104	21	AAW28787	Arbidopsia thalia
297	6	1.8	68	22	AAW31223	Novel human secret	370	6	1.8	104	22	AAW93150	Human digestive sy
298	6	1.8	69	19	AAW62767	Streptococcus pneu	371	6	1.8	104	22	AAW09976	Human polypeptide
299	6	1.8	70	22	AAW61615	Propionibacterium	372	6	1.8	105	21	AAW09341	Arbidopsia thalia
300	6	1.8	70	22	AAW39362	Peptide #6868 enco	373	6	1.8	105	22	AAW01436	Novel human diagno
301	6	1.8	70	22	AAW24153	Protein #6152 enco	374	6	1.8	105	22	AAW12235	Human secreted pro
302	6	1.8	70	22	AAW60040	Human brain expres	375	6	1.8	106	21	AAW38617	Arbidopsia thalia
303	6	1.8	70	22	AAW72643	Human bone marrow	376	6	1.8	106	22	AAW15277	Novel human diagno

377	6	1.8	106	22	ABG18692	Novel human diagno	450	6	1.8	148	18	AAW31606	Calcitonin gene re
378	6	1.8	106	22	AAO01772	Human polypeptide	451	6	1.8	148	19	AAW46487	Human calcitonin g
379	6	1.8	107	10	AAAP5449	Sequence encoded b	452	6	1.8	148	19	AAW50004	Human CGRP-RCF. H
380	6	1.8	107	22	ABBI7511	Human nervous syst	453	6	1.8	148	22	AAU60882	Protonibacterium
381	6	1.8	111	22	AAO09691	Human polypeptide	454	6	1.8	148	22	ABG07704	Novel human diagno
382	6	1.8	111	22	AAW34490	Human EST encoded	455	6	1.8	148	22	AAU32258	Novel human secret
383	6	1.8	112	21	AAW02448	Human secreted pro	456	6	1.8	149	20	AAU07982	Human secreted pro
384	6	1.8	115	21	AAU9075	Zea mays protein f	457	6	1.8	149	20	ABG17169	Novel human diagno
385	6	1.8	115	22	AAU73666	Human colon cancer	458	6	1.8	150	22	ABG68625	Drosophila melanog
386	6	1.8	116	22	AAU49869	Protonibacterium	459	6	1.8	151	22	ABG29326	Novel human diagno
387	6	1.8	116	22	AAO10137	Human polypeptide	460	6	1.8	151	22	AAU01415	Latex allergen Hev
388	6	1.8	116	22	AAU91102	C glutamicum prote	461	6	1.8	152	19	AAW73158	Human amphiregulin
389	6	1.8	117	22	AAU91996	C glutamicum prote	462	6	1.8	152	22	AAU47645	Protonibacterium
390	6	1.8	117	22	ABB70510	Drosophila melanog	463	6	1.8	154	21	AAW98259	H. pylori GHP0 895
391	6	1.8	117	22	AAU24083	A pernix EST encod	464	6	1.8	154	21	AAU91902	Zea mays protein f
392	6	1.8	118	22	AAU58221	Arbidiopsis thalia	465	6	1.8	155	15	AAU45451	Adenovirus E1A-F p
393	6	1.8	119	22	ABG06840	Novel human diagno	466	6	1.8	155	21	AAU37515	Arbidiopsis thalia
394	6	1.8	119	22	AAU85550	Human immune/haema	467	6	1.8	155	22	AAU49551	Protonibacterium
395	6	1.8	120	20	AAU93160	Human Lefty-2 prot	468	6	1.8	155	22	AAU56458	Protonibacterium
396	6	1.8	120	21	AAU76113	Arbidiopsis thalia	469	6	1.8	155	22	AAU41768	Human polypeptide
397	6	1.8	122	18	AAU4565	Streptococcus pneu	470	6	1.8	155	22	AAU68931	Neisseria meningit
398	6	1.8	122	21	AAU94757	Yeast YJL011CP que	471	6	1.8	155	22	AAU42036	Human polypeptide
399	6	1.8	124	18	AAU14582	Streptococcus pneu	472	6	1.8	157	22	AAU62368	Solidie Human ampn
400	6	1.8	124	21	AAU34366	Gene 10 human secr	473	6	1.8	158	19	AAU73156	Protonibacterium
401	6	1.8	124	21	AAU76113	Murine cell wall p	474	6	1.8	158	22	AAU93656	Protonibacterium
402	6	1.8	124	22	AAU56052	Skin cell protein,	475	6	1.8	158	22	AAU44918	Peptide #7364 enco
403	6	1.8	128	18	AAU14577	Streptococcus pneu	476	6	1.8	158	22	AAU39858	Peptide #7364 enco
404	6	1.8	128	18	AAU14577	Human secreted pro	477	6	1.8	158	22	AAU60590	Human brain expres
405	6	1.8	128	18	AAU14577	Human secreted pro	478	6	1.8	158	22	AAU73258	Human bone marrow
406	6	1.8	128	18	AAU14577	Human secreted pro	479	6	1.8	158	22	AAU19901	Peptide #6335 enco
407	6	1.8	129	22	AAU06247	Human polypeptide	480	6	1.8	158	22	AAU33459	C glutamicum prote
408	6	1.8	129	22	AAU92877	Human protein sequ	481	6	1.8	158	22	AAU79007	Sequence of human
409	6	1.8	130	20	AAU15226	Human receptor pro	482	6	1.8	158	22	AAU79007	E. coli K12B prote
410	6	1.8	130	20	AAU44186	Protonibacterium	483	6	1.8	158	22	AAU31583	Drosophila melanog
411	6	1.8	131	18	AAU14583	Streptococcus pneu	484	6	1.8	159	8	AAU70494	Streptococcus pneu
412	6	1.8	131	20	AAU59718	Secreted protein 7	485	6	1.8	159	21	AAU11368	Protonibacterium
413	6	1.8	131	22	AAU64639	Arbidiopsis thalia	486	6	1.8	159	21	AAU79301	Novel human diagno
414	6	1.8	131	22	AAU64639	Human secreted pro	487	6	1.8	159	21	AAU79301	E. coli phosphopan
415	6	1.8	132	21	AAU00109	Human secreted pro	488	6	1.8	159	22	AAU37770	Drosophila melanog
416	6	1.8	133	22	AAU19681	Novel human diagno	489	6	1.8	161	22	AAU38022	Streptococcus pneu
417	6	1.8	133	22	AAU87567	Human immune/haema	490	6	1.8	161	22	AAU42760	Protonibacterium
418	6	1.8	133	22	AAU02565	Human polypeptide	491	6	1.8	161	22	AAU56873	Protonibacterium
419	6	1.8	134	18	AAU14585	Streptococcus pneu	492	6	1.8	161	22	AAU23981	Novel human diagno
420	6	1.8	134	21	AAU75490	Neisseria meningit	493	6	1.8	161	22	AAU01086	Novel human diagno
421	6	1.8	134	21	AAU68574	Human novel cytoxi	494	6	1.8	161	22	AAU19602	S. pneumoniae deri
422	6	1.8	136	21	AAU56611	Human prostate can	495	6	1.8	163	19	AAU85871	Arbidiopsis thalia
423	6	1.8	136	22	AAU28035	Novel human diagno	496	6	1.8	163	21	AAU12155	Human nucleic acid
424	6	1.8	137	21	AAU19093	Zea mays protein f	497	6	1.8	164	21	AAU21038	Protonibacterium
425	6	1.8	137	22	AAU25517	Human protein sequ	498	6	1.8	164	22	AAU53362	Protonibacterium
426	6	1.8	138	21	AAU52184	Human secreted pro	499	6	1.8	164	22	AAU39982	Human polypeptide
427	6	1.8	138	22	AAU95453	Human reproductive	500	6	1.8	164	22	AAU39982	Human protein sequ
428	6	1.8	139	22	AAU19643	SEQ ID NO 361 from	501	6	1.8	165	22	AAU36392	Pseudomonas aerugi
429	6	1.8	139	21	AAU75491	Neisseria meningit	502	6	1.8	166	21	AAU30424	Arbidiopsis thalia
430	6	1.8	139	21	AAU75513	Neisseria meningit	503	6	1.8	166	22	AAU94660	Human protein sequ
431	6	1.8	139	21	AAU75514	Human reproductive	504	6	1.8	167	22	AAU22443	Novel human diagno
432	6	1.8	139	22	AAU96463	Human polypeptide	505	6	1.8	168	22	AAU16951	Human novel secret
433	6	1.8	139	22	AAU0250	Human polypeptide	506	6	1.8	169	22	AAU04715	Novel human diagno
434	6	1.8	139	22	AAU36627	Human FLEKHT-49 pr	507	6	1.8	172	21	AAU55367	Arbidiopsis thalia
435	6	1.8	140	22	AAU15342	Human polypeptide	508	6	1.8	172	21	AAU55367	Human colon cancer
436	6	1.8	140	22	AAU01291	Arbidiopsis thalia	509	6	1.8	174	21	AAU11477	Arbidiopsis thalia
437	6	1.8	141	21	AAU17012	Arbidiopsis thalia	510	6	1.8	175	19	AAU77365	Arbidiopsis thalia
438	6	1.8	141	21	AAU30425	Arbidiopsis thalia	511	6	1.8	175	19	AAU37844	Human XAG growth f
439	6	1.8	141	21	AAU37516	Arbidiopsis thalia	512	6	1.8	175	19	AAU37844	Human protein comp
440	6	1.8	141	21	AAU01016	Arbidiopsis thalia	513	6	1.8	175	20	AAU59675	Secreted protein 1
441	6	1.8	144	21	AAU09421	Arbidiopsis thalia	514	6	1.8	175	21	AAU24070	Human PRO1030 prot
442	6	1.8	144	21	AAU11806	Arbidiopsis thalia	515	6	1.8	175	21	AAU30423	Arbidiopsis thalia
443	6	1.8	144	21	AAU24084	Arbidiopsis thalia	516	6	1.8	175	21	AAU54995	Protonibacterium
444	6	1.8	144	21	AAU53630	Arbidiopsis thalia	517	6	1.8	175	22	AAU08804	Breast cancer cell
445	6	1.8	144	22	AAU10993	Human Ser/Thr kina	518	6	1.8	175	22	AAU72203	Human huxAG-1/CCSG
446	6	1.8	145	20	AAU37698	Chlamydia trachoma	519	6	1.8	176	21	AAU26108	Zea mays protein f
447	6	1.8	145	22	AAU63250	Protonibacterium	520	6	1.8	178	21	AAU11476	Arbidiopsis thalia
448	6	1.8	146	18	AAU31604	Calcitonin gene re	521	6	1.8	178	21	AAU11476	Novel human diagno
449	6	1.8	146	19	AAU73159	Human amphiregulin	522	6	1.8	179	22	AAU57428	Protonibacterium

523	6	1.8	180	18	AAW14562	Streptococcus pneu	596	6	1.8	219	22	AAW92035	C glutamicum prote
524	6	1.8	180	19	AAW98570	H. pylori GHPO 9 p	597	6	1.8	220	21	AAW13569	Streptomyces globi
525	6	1.8	180	21	AAW91357	Human secreted pro	598	6	1.8	220	21	AAW13569	Streptomyces globi
526	6	1.8	181	22	AAU33595	Pseudomonas aerugi	599	6	1.8	221	21	AAW17187	Eucalyptus grandis
527	6	1.8	184	18	AAW14589	Streptococcus pneu	600	6	1.8	221	21	AAW52743	Arabidopsis thalia
528	6	1.8	184	21	AAW16320	Eucalyptus grandis	601	6	1.8	222	21	AAW32874	Pinus radiata tren
529	6	1.8	184	22	AAW20257	White spot syndrom	602	6	1.8	222	18	AAW36796	Novel human protei
530	6	1.8	185	14	AAW34717	Bacillus subtilis	603	6	1.8	226	19	AAW73157	Human amphiregulin
531	6	1.8	185	18	AAW14566	Streptococcus pneu	604	6	1.8	227	22	AAU25579	Human G Protein-Co
532	6	1.8	186	22	ABG09410	Novel human diagno	605	6	1.8	228	21	AAW56645	Human prostate can
533	6	1.8	186	22	AAU17024	Human novel secret	606	6	1.8	228	21	AAW24362	Arabidopsis thalia
534	6	1.8	187	18	AAW14579	Streptococcus pneu	607	6	1.8	228	22	AAU43682	Propionibacterium
535	6	1.8	187	21	AAW29045	Arabidopsis thalia	608	6	1.8	230	22	AAU41712	Propionibacterium
536	6	1.8	187	22	AAU18421	Human endocrine po	609	6	1.8	231	21	AAW57995	Arabidopsis thalia
537	6	1.8	188	18	AAW14580	Streptococcus pneu	610	6	1.8	231	21	AAW61574	Arabidopsis thalia
538	6	1.8	189	21	AAW33435	Zea mays protein f	611	6	1.8	232	22	ABG12639	Novel human diagno
539	6	1.8	191	19	AAW38543	S. pneumoniae cyst	612	6	1.8	233	18	AAW14572	Streptococcus pneu
540	6	1.8	191	22	AAU54775	Propionibacterium	613	6	1.8	233	18	AAW14590	Streptococcus pneu
541	6	1.8	192	21	AAW91976	Mutline interferon	614	6	1.8	234	21	AAW30349	Arabidopsis thalia
542	6	1.8	192	22	AAW19975	Novel human diagno	615	6	1.8	236	21	AAW41465	Human ORFX ORF1229
543	6	1.8	193	22	AAU04899	Micromonospora eve	616	6	1.8	237	21	AAW23623	Arabidopsis thalia
544	6	1.8	193	22	AAU15093	Protein encoded by	617	6	1.8	237	22	AAU14095	Epsilon-Barr virus
545	6	1.8	194	20	AAW16590	Human ovarian tumo	618	6	1.8	240	21	AAW17333	Arabidopsis thalia
546	6	1.8	195	18	AAW14591	Streptococcus pneu	619	6	1.8	240	21	AAW30348	Arabidopsis thalia
547	6	1.8	195	20	AAW07105	Colon cancer assoc	620	6	1.8	240	22	AAW90252	Human immune/haema
548	6	1.8	195	21	AAW29044	Arabidopsis thalia	621	6	1.8	240	22	AAW66648	Mouse tissue facto
549	6	1.8	196	18	AAW14564	Streptococcus pneu	622	6	1.8	241	21	AAW66591	Arabidopsis thalia
550	6	1.8	197	21	AAW55366	Arabidopsis thalia	623	6	1.8	241	22	AAW58090	Drosophila melanog
551	6	1.8	197	22	AAW28941	Novel human diagno	624	6	1.8	241	22	AAW58090	Novel human diagno
552	6	1.8	197	22	AAW93076	C glutamicum prote	625	6	1.8	241	22	AAW90909	Novel human diagno
553	6	1.8	198	18	AAW14581	Streptococcus pneu	626	6	1.8	245	12	AAW11712	Human stem cell Pa
554	6	1.8	198	22	AAW28289	Novel human secret	627	6	1.8	245	13	AAW20646	Human "Delta 28" m
555	6	1.8	199	14	AAW3885	Consensus sequence	628	6	1.8	245	16	AAW83979	Human stem cell fa
556	6	1.8	199	22	AAW05326	Novel human diagno	629	6	1.8	245	22	AAW05267	Human SCF protei
557	6	1.8	199	22	AAW17356	Novel human diagno	630	6	1.8	245	22	AAW98368	Human SCF protei
558	6	1.8	199	22	AAW00086	Alpha-glucosidase	631	6	1.8	245	22	AAW02461	Human SCF protei
559	6	1.8	200	14	AAW43879	C-terminal portion	632	6	1.8	245	22	AAW02767	Human SCF protei
560	6	1.8	200	21	AAW55365	Arabidopsis thalia	633	6	1.8	245	22	AAW73568	Human SCF protei
561	6	1.8	200	22	AAW14506	Novel human diagno	634	6	1.8	245	22	AAW96953	Human stem cell fa
562	6	1.8	202	22	AAW05621	Human colon cancer	635	6	1.8	246	20	AAW34805	Chlamydia pneumoni
563	6	1.8	203	21	AAW09340	Arabidopsis thalia	636	6	1.8	246	21	AAW53285	Human SCF protei
564	6	1.8	204	18	AAW14571	Streptococcus pneu	637	6	1.8	247	19	AAW73160	Human SCF protei
565	6	1.8	204	18	AAW14578	Streptococcus pneu	638	6	1.8	248	21	AAW54570	Zea mays protein f
566	6	1.8	204	21	AAW38616	Arabidopsis thalia	639	6	1.8	248	22	AAW67745	Amino acid sequenc
567	6	1.8	204	22	AAW84978	Shrimp white spot	640	6	1.8	250	14	AAW38794	Monoglyceride 11pa
568	6	1.8	204	22	AAW20261	White spot syndrom	641	6	1.8	250	22	AAW61109	Drosophila melanog
569	6	1.8	205	21	AAW41610	Human ORFX ORF1374	642	6	1.8	251	21	AAW43216	Human ORFX ORF2980
570	6	1.8	205	21	AAW23624	Arabidopsis thalia	643	6	1.8	251	21	AAW16274	Eucalyptus grandis
571	6	1.8	205	22	AAW91597	C glutamicum prote	644	6	1.8	251	22	AAW00658	Novel human diagno
572	6	1.8	206	20	AAW73837	Human prostate tum	645	6	1.8	251	22	AAW08208	Novel human diagno
573	6	1.8	206	22	AAW05794	Novel human diagno	646	6	1.8	252	10	AAW95447	Amphiregulin precu
574	6	1.8	206	22	AAW95820	Human protein sequ	647	6	1.8	253	22	AAW48839	Petunia hybrida zp
575	6	1.8	207	22	AAW09882	Human human diagno	648	6	1.8	254	22	AAW26078	Novel human diagno
576	6	1.8	208	21	AAW95314	Corri phosphatidylg	649	6	1.8	257	21	AAW22406	Arabidopsis thalia
577	6	1.8	208	21	AAW68968	Cps25 protein whic	650	6	1.8	257	21	AAW54569	Zea mays protein f
578	6	1.8	208	22	AAW95022	Human protein sequ	651	6	1.8	258	12	AAW15227	HincII modificatio
579	6	1.8	209	22	AAW67923	Propionibacterium	652	6	1.8	258	19	AAW55107	Streptococcus pneu
580	6	1.8	211	22	AAW52836	Propionibacterium	653	6	1.8	258	21	AAW34197	Gene 35 human secr
581	6	1.8	211	22	AAW12080	Dendritic cell (DC	654	6	1.8	259	21	AAW17186	Arabidopsis thalia
582	6	1.8	212	21	AAW57996	Arabidopsis thalia	655	6	1.8	259	21	AAW52742	Arabidopsis thalia
583	6	1.8	212	21	AAW61575	Arabidopsis thalia	656	6	1.8	260	11	AAW08332	Pseudomonas creati
584	6	1.8	212	22	AAW03224	Novel human diagno	657	6	1.8	260	17	AAW03520	Bali restriction e
585	6	1.8	212	22	AAW05311	Novel human diagno	658	6	1.8	260	21	AAW40773	Zea mays protein f
586	6	1.8	212	22	AAW05798	Novel human diagno	659	6	1.8	260	22	AAW57988	Drosophila melanog
587	6	1.8	213	22	AAW02504	Novel human diagno	660	6	1.8	263	21	AAW11475	Arabidopsis thalia
588	6	1.8	213	22	AAW84215	Amino acid sequenc	661	6	1.8	263	22	AAW64191	Drosophila melanog
589	6	1.8	214	22	AAW84647	Cryptocoditulum sp	662	6	1.8	263	22	AAW25283	Novel human diagno
590	6	1.8	214	22	AAW97225	Mutline C-type lect	663	6	1.8	264	22	AAW55613	Propionibacterium
591	6	1.8	217	21	AAW41828	Arabidopsis thalia	664	6	1.8	265	20	AAW29128	Amino acid sequenc
592	6	1.8	218	22	AAW58170	Propionibacterium	665	6	1.8	266	22	AAW00609	Novel human diagno
593	6	1.8	218	22	AAW12079	Dendritic cell (DC	666	6	1.8	266	22	AAW03074	Novel human diagno
594	6	1.8	219	21	AAW17011	Arabidopsis thalia	667	6	1.8	266	22	AAW06836	Novel human diagno
595	6	1.8	219	21	AAW41827	Arabidopsis thalia	668	6	1.8	266	22	AAW05263	Stem cell factor (

669	6	1.8	265	22	AA682440	S. epidermidis ope	742	6	1.8	303	22	ABG14308	Novel human diagno
670	6	1.8	266	22	AA68365	Consensus SCF prot	743	6	1.8	305	21	AA605380	Arabidopsis thalia
671	6	1.8	266	22	AAU02490	SCF (stem cell fac	744	6	1.8	305	21	AA630828	Arabidopsis thalia
672	6	1.8	266	22	AAU02776	SCF (stem cell fac	745	6	1.8	305	21	AA648337	Arabidopsis thalia
673	6	1.8	266	22	AA696950	Stem cell factor S	746	6	1.8	305	22	AA62463	Fruit fly Cnki kin
674	6	1.8	267	22	AAU14624	Novel bone marrow	747	6	1.8	305	22	AA694143	Human protein sequ
675	6	1.8	269	22	AA685801	Human GTP-binding	748	6	1.8	307	20	AA659886	Human normal uteru
676	6	1.8	270	21	AA644663	Zea mays protein f	749	6	1.8	307	22	AA619420	A prenyltransferas
677	6	1.8	272	21	AA640772	Zea mays protein f	750	6	1.8	307	22	AA681714	S. epidermidis ope
678	6	1.8	273	12	AA611711	Human Stem Cell fa	751	6	1.8	309	21	AA654568	Zea mays protein f
679	6	1.8	273	13	AA620647	Human mast cell gr	752	6	1.8	309	21	AA654568	Escherichia coli f
680	6	1.8	273	14	AA632166	hKL fragment A, S	753	6	1.8	309	22	AA636124	Klebsiella pneumon
681	6	1.8	273	16	AA683978	Human stem cell fa	754	6	1.8	309	22	AA636124	Novel human diagno
682	6	1.8	273	18	AA627607	Human recombinant	755	6	1.8	309	22	AA636124	Novel human diagno
683	6	1.8	273	21	AA653284	Human SCF protein	756	6	1.8	309	22	AA636124	Novel human diagno
684	6	1.8	273	22	AAU05256	Human stem cell fa	757	6	1.8	310	21	AA636124	Novel human diagno
685	6	1.8	273	22	AAU05266	Human SCF protein	758	6	1.8	310	21	AA645676	Arabidopsis thalia
686	6	1.8	273	22	AA698356	Human stem cell fa	759	6	1.8	310	22	AA605654	Novel human diagno
687	6	1.8	273	22	AA698357	Human SCF protein	760	6	1.8	311	22	AA605654	Novel human diagno
688	6	1.8	273	22	AA698357	Human SCF protein	761	6	1.8	312	21	AA651729	Arabidopsis thalia
689	6	1.8	273	22	AAU02458	Human SCF (stem ce	762	6	1.8	313	7	AA650071	Sequence of the Tr
690	6	1.8	273	22	AAU02460	Human SCF (stem ce	763	6	1.8	313	22	AA630282	Novel human diagno
691	6	1.8	273	22	AAU02765	Human SCF (stem ce	764	6	1.8	314	15	AA654664	I kappa B like pro
692	6	1.8	273	22	AAU02766	Human SCF protein	765	6	1.8	314	20	AA636124	Protein involved i
693	6	1.8	273	22	AA673566	Human SCF (stem ce	766	6	1.8	314	21	AA636124	Euclalyptus grandis
694	6	1.8	273	22	AA673567	Human SCF protein	767	6	1.8	314	21	AA636124	Protonibacterium
695	6	1.8	273	22	AA696941	Human stem cell fa	768	6	1.8	315	21	AA636124	Arabidopsis thalia
696	6	1.8	273	22	AA696942	Human stem cell fa	769	6	1.8	315	22	AA636124	Human olfactory re
697	6	1.8	273	22	AA696952	Human stem cell fa	770	6	1.8	316	21	AA636124	Arabidopsis thalia
698	6	1.8	274	22	AA600718	Novel human diagno	771	6	1.8	316	22	AA627974	Arabidopsis thalia
699	6	1.8	274	22	AA670071	Human secreted pro	772	6	1.8	316	22	AA627974	Arabidopsis thalia
700	6	1.8	275	20	AA687603	Preproagmatin seq	773	6	1.8	316	22	AA627974	Arabidopsis thalia
701	6	1.8	276	20	AA637171	Amino acid sequenc	774	6	1.8	317	21	AA636590	Drosophila melano
702	6	1.8	276	22	AA659768	Drosophila melano	775	6	1.8	317	21	AA636590	Human polyptide
703	6	1.8	278	22	AA65782	Cysteine protease	776	6	1.8	317	21	AA636590	Arabidopsis thalia
704	6	1.8	280	19	AA654379	Cell division cycl	777	6	1.8	317	22	AA624318	Arabidopsis thalia
705	6	1.8	281	20	AA697119	S-adenosyl-L-methy	778	6	1.8	318	21	AA648300	Novel human diagno
706	6	1.8	281	21	AA694924	Human secreted pro	779	6	1.8	320	21	AA613407	Arabidopsis thalia
707	6	1.8	282	20	AA667850	Human secreted pro	780	6	1.8	321	21	AA618723	Arabidopsis thalia
708	6	1.8	282	21	AA641826	Arabidopsis thalia	781	6	1.8	321	21	AA675552	A Neisseria mening
709	6	1.8	283	22	AA612979	Port tapeworm matu	782	6	1.8	321	21	AA675552	Neisseria meningit
710	6	1.8	284	20	AA637002	Chlamydia trachoma	783	6	1.8	322	22	AA666009	Drosophila melano
711	6	1.8	284	22	AA628101	Novel human secret	784	6	1.8	323	21	AA675550	Neisseria gonorrhoe
712	6	1.8	284	22	AA625837	Human protein sequ	785	6	1.8	323	22	AA656092	Protonibacterium
713	6	1.8	284	22	AA693250	Human protein HP02	786	6	1.8	323	22	AA656092	Novel human secret
714	6	1.8	286	21	AA653041	Human secreted pro	787	6	1.8	324	21	AA632466	Human secreted pro
715	6	1.8	286	22	AAU05263	Human protein SEQ	788	6	1.8	324	21	AA617331	Arabidopsis thalia
716	6	1.8	286	22	AAU05263	Human protein SEQ	789	6	1.8	324	22	AA617331	Novel human diagno
717	6	1.8	287	21	AA644642	Zea mays protein f	790	6	1.8	325	21	AA619095	Protein encoded by
718	6	1.8	287	22	AA653597	C glutamicum prote	791	6	1.8	325	21	AA635795	Arabidopsis thalia
719	6	1.8	287	22	AA690436	S. epidermidis ope	792	6	1.8	325	21	AA635795	Arabidopsis thalia
720	6	1.8	288	21	AA695834	Porcine adenovirus	793	6	1.8	325	21	AA635795	Haemophilus influe
721	6	1.8	288	22	AA659523	Drosophila melano	794	6	1.8	326	19	AA636585	Novel human diagno
722	6	1.8	288	22	AA653040	Escherichia coli p	795	6	1.8	326	22	AA600257	Peptide #2792 enco
723	6	1.8	288	22	AA673577	Arabidopsis thalia	796	6	1.8	326	22	AA630141	Peptide #2817 enco
724	6	1.8	290	13	AA628774	Consensus SCF (ste	797	6	1.8	326	22	AA635311	Human brain expres
725	6	1.8	290	13	AA628774	MD66 Marek's Disea	798	6	1.8	326	22	AA656142	Human bone marrow
726	6	1.8	290	22	AA612877	Port tapeworm matu	799	6	1.8	326	22	AA656142	Peptide #2753 enco
727	6	1.8	290	22	AA612877	Port tapeworm matu	800	6	1.8	326	22	AA656142	Peptide #2753 enco
728	6	1.8	292	22	AA605275	Novel human diagno	801	6	1.8	326	22	AA616319	Human colon cancer
729	6	1.8	294	22	AA662954	Drosophila melano	802	6	1.8	326	22	AA628814	Hybrid trpE-SS14 P
730	6	1.8	294	22	AA617361	Novel human diagno	803	6	1.8	326	22	AA640057	Haemophilus influe
731	6	1.8	294	22	AA635940	TGF-beta 4 amino a	804	6	1.8	326	22	AA675109	Peptide #2739 enco
732	6	1.8	295	21	AA628761	Arabidopsis thalia	805	6	1.8	327	6	AA650046	Human colon cancer
733	6	1.8	295	21	AA628761	Arabidopsis thalia	806	6	1.8	327	6	AA650046	Hybrid trpE-SS14 P
734	6	1.8	296	22	AA692212	C glutamicum prote	807	6	1.8	327	22	AA699096	Rat GnRH receptor
735	6	1.8	298	21	AA651730	Arabidopsis thalia	808	6	1.8	327	22	AA699097	Rat GnRH receptor
736	6	1.8	299	19	AA661008	Streptococcus pneu	809	6	1.8	327	22	AA699098	Rat GnRH receptor
737	6	1.8	299	20	AA649158	Corn cyclin-depend	810	6	1.8	327	22	AA699099	Rat GnRH receptor
738	6	1.8	300	22	AA658826	Drosophila melano	811	6	1.8	327	22	AA699100	Rat GnRH receptor
739	6	1.8	301	22	AAU04700	Protonibacterium	812	6	1.8	327	22	AA662501	Rat GnRH receptor
740	6	1.8	302	22	AA604249	Novel human diagno	813	6	1.8	327	22	AA662502	Rat GnRH receptor
741	6	1.8	303	22	AA658168	Drosophila melano	814	6	1.8	327	22	AA662503	Rat GnRH receptor

815	6	1.8	327	22	AA62504	Rat GnRH receptor	888	6	1.8	361	22	ABG05318	Novel human diagno
816	6	1.8	328	17	AAW91225	Human placenta G-p	889	6	1.8	362	20	AAV35611	Chlamydia pneumoni
817	6	1.8	328	18	AAW09433	Human placenta pur	890	6	1.8	362	21	AAW09440	Arabisdopsis thaila
818	6	1.8	328	21	AAW53596	Arabisdopsis thaila	891	6	1.8	362	21	AAW45208	Arabisdopsis thaila
819	6	1.8	328	22	AAW5932	H. influenzae zipa	892	6	1.8	362	22	AAW93137	C glutamicum prote
820	6	1.8	328	22	AAW04393	Human p2-purifier	893	6	1.8	363	22	AAW62107	Drosophila melanog
821	6	1.8	329	21	AAW35796	Protein Involved I	894	6	1.8	363	22	AAW96616	Putative P. abysal
822	6	1.8	329	22	AAW72696	Murine OR-Like pol	895	6	1.8	365	20	AAW02005	Enterococcus faeca
823	6	1.8	330	21	AAW13406	Human ataxin-2 bin	896	6	1.8	365	22	AAW04631	Novel human diagno
824	6	1.8	330	21	AAW81462	Human ataxin-2 bin	897	6	1.8	365	22	AAW34503	Human gene 30-enco
825	6	1.8	331	20	AAW50338	P. fluorescens ICS	898	6	1.8	366	20	AAW17871	Human bone morphog
826	6	1.8	331	20	AAW14919	Amino acid sequenc	899	6	1.8	366	21	AAW30826	Arabisdopsis thaila
827	6	1.8	331	22	AAW18006	Novel human diagno	900	6	1.8	366	21	AAW33595	Arabisdopsis thaila
828	6	1.8	332	21	AAW30827	Arabisdopsis thaila	901	6	1.8	366	22	AAW95157	Human protein sequ
829	6	1.8	333	22	AAW31751	Novel human secret	902	6	1.8	366	22	AAW19837	Endometrial bleed
830	6	1.8	333	22	AAW79218	Corynebacterium q1	903	6	1.8	367	22	AAW05310	Novel human diagno
831	6	1.8	334	22	AAW71970	Drosophila melanog	904	6	1.8	367	22	AAW05795	Novel human diagno
832	6	1.8	334	22	AAW34788	E. coli cellular p	905	6	1.8	367	22	AAW00875	Human cancer relat
833	6	1.8	335	21	AAW29000	Arabisdopsis thaila	906	6	1.8	369	21	AAW14169	Arabisdopsis thaila
834	6	1.8	335	22	AAW30843	Novel human secret	907	6	1.8	369	21	AAW27430	Arabisdopsis thaila
835	6	1.8	337	21	AAW74311	Neisseria gonorrhoe	908	6	1.8	370	15	AAW48697	G-protein coupled
836	6	1.8	337	22	AAW34091	Staphylococcus aur	909	6	1.8	370	17	AAW02669	Human protein coupld
837	6	1.8	337	22	AAW38207	Salmonella typhi c	910	6	1.8	370	21	AAW92013	Human transforming
838	6	1.8	337	22	AAW10588	Novel human diagno	911	6	1.8	371	21	AAW28999	Arabisdopsis thaila
839	6	1.8	339	22	AAW28871	Novel human diagno	912	6	1.8	372	20	AAW07102	Colon cancer assoc
840	6	1.8	339	22	AAW68530	Human novel cytoxi	913	6	1.8	372	21	AAW09439	Arabisdopsis thaila
841	6	1.8	340	22	AAW68532	Staphylococcus aur	914	6	1.8	372	21	AAW45207	Arabisdopsis thaila
842	6	1.8	340	22	AAW37545	Staphylococcus aur	915	6	1.8	372	22	AAW92376	C glutamicum prote
843	6	1.8	343	21	AAW27973	Arabisdopsis thaila	916	6	1.8	374	12	AAW13987	Lycopene cyclase -
844	6	1.8	344	22	AAW16460	Human novel secret	917	6	1.8	374	17	AAW01125	Lycopene cyclase.
845	6	1.8	344	22	AAW72994	Olfactory receptor	918	6	1.8	374	18	AAW32474	Ervinia herbicola
846	6	1.8	345	21	AAW14170	Arabisdopsis thaila	919	6	1.8	375	21	AAW28998	Arabisdopsis thaila
847	6	1.8	345	21	AAW27431	Arabisdopsis thaila	920	6	1.8	376	12	AAW15272	Fusarium oxysporum
848	6	1.8	345	22	AAW65931	Alpha-actin zipa p	921	6	1.8	376	13	AAW25527	Fusarium oxysporum
849	6	1.8	345	22	AAW92830	C glutamicum prote	922	6	1.8	376	13	AAW25466	Endoglucanase #2.
850	6	1.8	346	22	AAW79347	Corynebacterium gl	923	6	1.8	376	13	AAW25429	Cellulase containe
851	6	1.8	346	22	AAW70516	Drosophila melanog	924	6	1.8	376	13	AAW27969	Endoglucanase enzy
852	6	1.8	347	22	AAW14105	Novel human diagno	925	6	1.8	376	14	AAW37151	Dye transfer inhib
853	6	1.8	347	22	AAW14470	Novel human diagno	926	6	1.8	376	14	AAW42064	Endoglucanase enzy
854	6	1.8	347	22	AAW14470	Novel human diagno	927	6	1.8	376	16	AAW67389	F. oxysporum endog
855	6	1.8	347	22	AAW61981	S. avermitilis ORF	928	6	1.8	376	19	AAW46617	Fusarium oxysporum
856	6	1.8	348	22	AAW48382	Propionibacterium	929	6	1.8	376	22	AAW35314	Enterococcus faeca
857	6	1.8	349	8	AAW70463	Sequence of gpi en	930	6	1.8	377	21	AAW27972	Arabisdopsis thaila
858	6	1.8	350	20	AAW02170	A Staphylococcus a	931	6	1.8	379	10	AAW90508	Sequence of an epi
859	6	1.8	350	21	AAW57994	Arabisdopsis thaila	932	6	1.8	380	10	AAW90509	Sequence of an epi
860	6	1.8	350	21	AAW61573	Arabisdopsis thaila	933	6	1.8	380	10	AAW90510	Sequence of an epi
861	6	1.8	350	22	AAW34216	Staphylococcus aur	934	6	1.8	380	10	AAW90511	Sequence of an epi
862	6	1.8	350	22	AAW36879	Staphylococcus aur	935	6	1.8	380	10	AAW90512	Sequence of new po
863	6	1.8	350	22	AAW65972	Propionibacterium	936	6	1.8	381	21	AAW22405	Arabisdopsis thaila
864	6	1.8	350	22	AAW65972	Novel human diagno	937	6	1.8	381	22	AAW35377	Haemophilus influe
865	6	1.8	351	21	AAW74312	Neisseria meningit	938	6	1.8	382	22	AAW64589	Drosophila melanog
866	6	1.8	352	18	AAW20628	H. pylori cytoplas	939	6	1.8	382	22	AAW03207	Novel human diagno
867	6	1.8	353	22	AAW68107	Drosophila melanog	940	6	1.8	383	19	AAW98461	H. pylori GHP0 718
868	6	1.8	353	22	AAW10861	Novel human diagno	941	6	1.8	383	21	AAW10770	Arabisdopsis thaila
869	6	1.8	354	20	AAW07104	Colon cancer assoc	942	6	1.8	386	22	AAW36377	Staphylococcus aur
870	6	1.8	354	21	AAW09441	Arabisdopsis thaila	943	6	1.8	386	22	AAW92871	C glutamicum prote
871	6	1.8	354	21	AAW45209	Arabisdopsis thaila	944	6	1.8	386	22	AAW79610	Corynebacterium gl
872	6	1.8	355	21	AAW75398	Neisseria meningit	945	6	1.8	386	22	AAW79611	Corynebacterium gl
873	6	1.8	355	21	AAW75399	Neisseria meningit	946	6	1.8	386	22	AAW80028	Corynebacterium gl
874	6	1.8	356	21	AAW30226	Arabisdopsis thaila	947	6	1.8	387	22	AAW10857	Novel human diagno
875	6	1.8	356	21	AAW34496	Arabisdopsis thaila	948	6	1.8	388	21	AAW06883	Arabisdopsis thaila
876	6	1.8	356	22	AAW65391	Propionibacterium	949	6	1.8	388	21	AAW45675	Arabisdopsis thaila
877	6	1.8	356	22	AAW65391	Streptococcus pyog	950	6	1.8	388	22	AAW18035	Novel human diagno
878	6	1.8	357	15	AAW04127	Fusarium oxysporum	951	6	1.8	390	21	AAW10769	Arabisdopsis thaila
879	6	1.8	357	22	AAW75397	Neisseria gonorrhoe	952	6	1.8	391	20	AAW50336	P. fluorescens ICS
880	6	1.8	357	22	AAW00023	Novel human diagno	953	6	1.8	391	22	AAW62644	Drosophila melanog
881	6	1.8	359	22	AAW05264	Novel human diagno	954	6	1.8	391	22	AAW90766	Human shear stress
882	6	1.8	359	22	AAW15053	Novel human diagno	955	6	1.8	392	20	AAW00204	Enterococcus faeca
883	6	1.8	359	22	AAW19795	Novel human diagno	956	6	1.8	392	22	AAW19861	Novel human diagno
884	6	1.8	359	22	AAW23276	Novel human diagno	957	6	1.8	393	21	AAW57000	Human prostate can
885	6	1.8	360	21	AAW32575	Eucalyptus grandis	958	6	1.8	395	21	AAW18686	Arabisdopsis thaila
886	6	1.8	360	22	AAW23283	Novel human diagno	959	6	1.8	396	21	AAW21215	cyC/Hpa44/HF fusio
887	6	1.8	361	22	AAW33906	Staphylococcus aur	960	6	1.8	396	22	AAW51015	Propionibacterium

961	6	1.8	397	21	AAB643211	Human ORFX ORF2975
962	6	1.8	397	21	AA606892	Arabidopsis thaliana
963	6	1.8	397	21	AA645674	Arabidopsis thaliana
964	6	1.8	397	22	AAB92573	Human protein sequ
965	6	1.8	398	21	AA618665	Arabidopsis thaliana
966	6	1.8	399	22	ABB660049	Drosophila melanog
967	6	1.8	399	22	ABB669710	Drosophila melanog
968	6	1.8	400	22	ABB668410	Drosophila melanog
969	6	1.8	400	22	ABG17359	Novel human diagnc
970	6	1.8	400	22	ABG22434	Novel human diagnc
971	6	1.8	402	11	AA805277	New serine hydroxy
972	6	1.8	402	11	AA614168	Arabidopsis thaliana
973	6	1.8	402	21	AA618684	Arabidopsis thaliana
974	6	1.8	402	21	AA627429	Arabidopsis thaliana
975	6	1.8	403	20	AAW97719	Staphylococcus aur
976	6	1.8	406	20	AA749152	Amnio acid sequenc
977	6	1.8	406	21	AAAB27154	H. pylori essential
978	6	1.8	407	22	AA691679	C glutaminc prote
979	6	1.8	408	19	AAW71465	Glycosyltransferas
980	6	1.8	408	21	AA767549	A. orientalis glycy
981	6	1.8	408	22	ABG22973	Novel human diagnc
982	6	1.8	409	19	AA711013	H. pylori ORF hp7e
983	6	1.8	409	19	AAW71464	Glycosyltransferas
984	6	1.8	409	21	AA757260	A. orientalis glycy
985	6	1.8	410	20	AA759966	Human endometrium
986	6	1.8	410	22	ABG22423	Novel human diagnc
987	6	1.8	412	20	AA749151	Amnio acid sequenc
988	6	1.8	413	22	AAU04815	Micromonospora eve
989	6	1.8	413	20	AA749139	Amnio acid sequenc
990	6	1.8	413	22	ABG08181	Novel human diagnc
991	6	1.8	414	21	AA675713	ATC6PK kinase doma
992	6	1.8	414	21	AA774313	Neisseria meningit
993	6	1.8	415	22	AAU37000	Staphylococcus aur
994	6	1.8	415	22	AAU37316	Staphylococcus aur
995	6	1.8	416	19	AAW98286	H. pylori GHPO 136
996	6	1.8	416	19	AAW60836	Human LAMP family
997	6	1.8	416	19	AAW50900	S. aureus histidin
998	6	1.8	416	20	AA729605	Human TSC403 prote
999	6	1.8	416	20	AAU35608	Helicobacter pylor
1000	6	1.8	416	22	AA694573	Human protein sequ

ALIGNMENTS

RESULT	1
AAW36984	
ID	AAW36984 standard; Protein; 328 AA.
XX	
AC	AAW36984;
XX	
DT	21-MAY-1998 (first entry)
XX	
DE	E. coli Z1PA protein useful in antimicrobial screening.
XX	
KW	Z1PA protein; antimicrobial; antibiotic; screening.
XX	
OS	Escherichia coli.
XX	
FH	Key
FT	Location/Qualifiers
FT	1..22
FT	/label= Sig-peptide
FT	4..13
FT	/note= "region of homology with H. influenzae
FT	Z1PA (Clam 16)"
FT	8..13
FT	/note= "region of homology with H. influenzae
FT	Z1PA (Clam 16)"
FT	8..20
FT	/note= "region of homology with H. influenzae
FT	Z1PA (Clam 16)"
FT	8..24
FT	/note= "region of homology with H. influenzae
FT	

Query Match	Best Local Similarity	100.0%;	Score 328;	DB 19;	Length 328;
Matches 328;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
1	MMQDLRLITLIVGAIATLILVHGFMFSRKERSMFPEDRLPKRKSKRDDSDYDEVDED 60				
1	mmqdlrlitlilvgaitatllivhgfmfsrkrersmfpedrpkrrksrdddsydevded 60				

PT for selection and design of inhibitors, potential antibacterial agents
 PS Disclosure; Fig 1B; 187pp; English.
 XX
 CC The invention provides a solution containing a C-terminal domain of
 CC E. coli Zlpa polypeptide. Zlpa is an integral membrane protein that is
 CC highly conserved among Gram-negative bacteria and essential for
 CC development of the septum during bacterial cell division. Crystalline
 CC Zlpa C-terminal fragment is used for design and selection of inhibitors
 CC of Zlpa. The inhibitors are potentially useful as antibacterials.
 CC effective against Gram-negative species. Sequences AAG65927-932 represent
 CC Zlpa protein sequences from various bacterial species.
 CC
 XX Sequence 328 AA:
 SQ
 Query Match 6.4%; Score 21; DB 22; Length 328;
 Best Local Similarity 100.0%; Pred. No. 1.2e-12;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 279 LQNFKLMLQSAQHIADEVGCV 299
 ||||||||||||||||
 Db 279 Lqnfklmlgsaqhadevgcv 299
 RESULT 6
 AAG65928
 ID AAG65928 standard; protein; 328 AA.
 XX
 AC AAG65928;
 XX
 DT 11-FEB-2002 (first entry)
 XX
 DE Y. pestis Zlpa protein sequence.
 XX
 KM Zlpa; Integral membrane protein; Gram-negative bacteria; antibacterial.
 XX
 OS Yersinia pestis.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1..328
 FT /note= "residues Xaa are unidentified"
 XX
 PN MO200173436-A1.
 XX
 PD 04-OCT-2001.
 XX
 PR 26-MAR-2001; 2001MO-US09826.
 PR
 PA 28-MAR-2000; 2000US-0536774.
 PA (AMHP) AMERICAN HOME PROD CORP.
 XX
 PI Glasfeld E, Moy FU, Powers R, Mosyak L, Somers WS;
 DR WPI; 2001-656940/75.
 XX
 PT C-terminal domain of Zlpa protein, in solution or crystal form, useful
 PT for selection and design of inhibitors, potential antibacterial agents
 PT
 PS Disclosure; Fig 1B; 187pp; English.
 XX
 CC The invention provides a solution containing a C-terminal domain of
 CC E. coli Zlpa polypeptide. Zlpa is an integral membrane protein that is
 CC highly conserved among Gram-negative bacteria and essential for
 CC development of the septum during bacterial cell division. Crystalline
 CC Zlpa C-terminal fragment is used for design and selection of inhibitors
 CC of Zlpa. The inhibitors are potentially useful as antibacterials,
 CC effective against Gram-negative species. Sequences AAG65927-932 represent
 CC Zlpa protein sequences from various bacterial species.
 CC

SQ Sequence 328 AA:
 Query Match 3.4%; Score 11; DB 22; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.015;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 242 LFSLANMKPG 252
 |||||||||
 Db 239 lfslanmkpg 249
 RESULT 7
 AAW81571
 ID AAW81571 standard; Protein; 522 AA.
 XX
 AC AAW81571;
 XX
 DT 01-MAR-1999 (first entry)
 XX
 DE Mus dunni endogenous virus Gag protein.
 XX
 KM MDEV; retrovirus; packaging cell line; gene transfer; gene therapy;
 KM vector; Gag protein.
 XX
 OS Mus dunni endogenous virus.
 XX
 PN MO9850538-A1.
 XX
 PD 12-NOV-1998.
 XX
 PE 08-MAY-1998; 98MO-US09452.
 XX
 PR 08-MAY-1998; 98US-0075272.
 PR 09-MAY-1997; 97US-0046140.
 XX
 PA (HUTC-) HUTCHINSON CANCER RES CENT FRED.
 XX
 PI Bonham L, Miller AD, Wolgamot G;
 DR WPI; 1999-034718/03.
 DR N-PSDB; AAV69750.
 XX
 PT New retroviral packaging cells - containing Mus dunni endogenous
 PT virus sequences to target cells, retrovirus gag and pol genes and a
 PT heterologous gene of interest.
 XX
 PS Disclosure; Page 67-68; 85pp; English.
 XX
 CC This is the amino acid sequence of the Gag protein of
 CC Mus dunni endogenous virus (MDEV), as deduced from the MDEV
 CC nucleotide sequence (see AAV69750). A cultured packaging cell is
 CC claimed which produces a replication-defective retroviral vector
 CC (RDRV) particle, where the packaging cell is a vertebrate cell
 CC capable of expressing and assembling retroviral proteins,
 CC comprising: (a) a first vector encoding a retroviral envelope
 CC protein having amino acid residues MDEV that direct binding of the
 CC retroviral particle to MDEV retroviral receptors on a target cell;
 CC and (b) a second vector encoding retrovirus gag and pol proteins,
 CC where upon expression of the vectors in the packaging cell in the
 CC presence of a vector having a sequence of a heterologous gene of
 CC interest, a replication-defective retroviral particle is produced
 CC that binds to MDEV receptors of target cells. Also claimed are:
 CC (1) a cultured packaging cell for producing a RDRV particle; (2)
 CC methods for producing a RDRV particle comprising a heterologous
 CC gene of interest; (3) cultured packaging cell line PD223; and (4) a
 CC RDRV produced by a method as in (2). The MDEV receptor is present
 CC on a variety of cells rendering MDEV pseudotype packaging cells
 CC useful in methods of mammalian and particularly human gene transfer
 CC for gene therapy. The MDEV packaging cells are a stable and
 CC reproducible source of retroviral particles. Clones may be
 CC isolated from these populations that produce high titre virus. The
 CC packaging cell lines may be selected and cloned for other desirable

CC properties, such as stability of in vivo growth, lack of production
 CC of helper virus, lack of reinfection by viral particles packaged in
 CC the cell, stability from genetic rearrangement and recombinational
 CC events, resistance to complement lysis, and improved ability to
 CC infect cells from higher mammals.
 XX
 SQ Sequence 522 AA;

Query Match 2.7%; Score 9; DB 20; Length 522;
 Best Local Similarity 100.0%; Pred. No. 2.3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 169 PVAAPOPEP 177
 DB 156 pvaapqpep 164

RESULT 8

AAW81570
 ID AAW81570 standard; Protein: 622 AA.

AAW81570;

01-MAR-1999 (first entry)

Mus dunni endogenous virus Gag protein (glycosylated).

MDEV; retrovirus; packaging cell line; gene transfer; gene therapy;
 vector; Gag protein.

Mus dunni endogenous virus.

Key Location/Qualifiers
 MISC-difference 1 /note="encoded by CTG"

MO9850538-A1.

12-NOV-1998.

08-MAY-1998; 98MO-US09452.

08-MAY-1998; 98US-0075272.

09-MAY-1997; 97US-0046140.

(HUTC-) HUTCHINSON CANCER RES CENT FRID.

Bonham L, Miller AD, Wolgemot G;

WPI: 1999-034718/03.

N-PSDB; AAV69750.

New retroviral packaging cells - containing Mus dunni endogenous
 virus sequences to target cells, retrovirus gag and pol genes and a
 heterologous gene of interest.

Disclosure: Page 65-66; 85pp; English.

This is the amino acid sequence of the glycosylated Gag protein of
 Mus dunni endogenous virus (MDEV), as deduced from the MDEV
 nucleotide sequence (see AAV69750). A cultured packaging cell is
 claimed which produces a replication-defective retroviral vector
 (RDV) particle, where the packaging cell is a vertebrate cell
 capable of expressing and assembling retroviral proteins,
 comprising: (a) a first vector encoding a retroviral envelope
 protein having amino acid residues MDEV that direct binding of the
 retroviral particle to MDEV retroviral receptors on a target cell;
 and (b) a second vector encoding retrovirus gag and pol proteins,
 where upon expression of the vectors in the packaging cell in the
 presence of a vector having a sequence of a heterologous gene of
 interest, a replication-defective retroviral particle is produced
 that binds to MDEV receptors of target cells. Also claimed are:

CC (1) a cultured packaging cell for producing a RDV particle; (2)
 CC methods for producing a RDV particle comprising a heterologous
 CC gene of interest; (3) cultured packaging cell line PD223; and (4) a
 CC RDV produced by a method as in (2). The MDEV receptor is present
 CC on a variety of cells rendering MDEV pseudotype packaging cells
 CC useful in methods of mammalian and particularly human gene transfer
 CC for gene therapy. The MDEV packaging cells are a stable and
 CC reproducible source of retroviral particles. Clones may be
 CC isolated from these populations that produce high titre virus. The
 CC packaging cell lines may be selected and cloned for other desirable
 CC properties, such as stability of in vivo growth, lack of production
 CC of helper virus, lack of reinfection by viral particles packaged in
 CC the cell, stability from genetic rearrangement and recombinational
 CC events, resistance to complement lysis, and improved ability to
 CC infect cells from higher mammals.
 XX
 SQ Sequence 622 AA;

Query Match 2.7%; Score 9; DB 20; Length 622;
 Best Local Similarity 100.0%; Pred. No. 2.7;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 169 PVAAPOPEP 177
 DB 256 pvaapqpep 264

RESULT 9

AAO03175
 ID AAO03175 standard; Protein: 36 AA.

AAO03175;

06-NOV-2001 (first entry)

Human polypeptide SEQ ID NO 17067.

Human; cytokine; cell proliferation; cell differentiation; gene therapy;
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KW tissue growth factor; immunomodulatory; cancer; leukaemia;
 KW nervous system disorders; arthritis; inflammation.

Homo sapiens.

WO200164835-A2.

07-SEP-2001.

26-FEB-2001; 2001MO-US04927.

28-FEB-2000; 2000US-0515126.

18-MAY-2000; 2000US-0577409.

(HYSE-) HYSO INC.

Tang YT, Liu C, Drmanac RT;

WPI: 2001-514838/56.

N-PSDB; AAI83106.

Isolated nucleic acids and polypeptides, useful for preventing
 PT diagnosing and treating e.g. leukaemia, inflammation and immune
 PT disorders.

Claim 20: SEQ ID NO 17067; 1399pp + Sequence Listing; English.

The invention relates to human polynucleotides (AAI79941-AAI93841) and
 CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,

CC e.g. stem cell growth factor activity, hematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 36 AA:

Query Match 2.4%; Score 8; DB 22; Length 36;
Best Local Similarity 100.0%; Pred. No. 2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 244 SLANMKP 251
Db 28 slankmkp 35
|||||||
|
RESULT 10
AA087430
ID AA087430 standard; Protein: 41 AA.
XX
AC AA087430;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human Immune/hematopoietic antigen SPQ ID NO:15023.
XX
KW Human; Immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytosolic; gene therapy; vaccine; metastasis.
XX
OS Homo sapiens.
XX
PN MO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205513.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225457.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226688.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229387.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 01-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 05-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234423.
PR 21-SEP-2000; 2000US-0234474.
PR 25-SEP-2000; 2000US-0234597.
PR 25-SEP-2000; 2000US-0234598.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237040.
PR 02-OCT-2000; 2000US-0237049.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.

PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0256719.
PR 08-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0253678.

XX (HUMA-) HUMAN GENOME SCI INC.
PA
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX MPI: 2001-483426/52.
DR N-PSTDB; AAK60211.
XX
XX
PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
PS Claim 11: SEQ ID NO 15023; 3071bp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK61921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (II)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (II)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK62169
CC represent sequences used in the exemplification of the present invention.

Sequence 41 AA:

Query Match	2.4%	Score 8;	DB 22;	Length 41;
Best Local Similarity	100.0%	Pred. No. 2.3;		
Matches 8;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	244	SLANKVKP	251	

Db	29	slanmwkp	36
RESULT	11		
AAOI3330			
ID	AAOI3330	standard; Protein; 42 AA.	
XX			
AC	AAOI3330;		
XX			
DT	06-NOV-2001	(first entry)	
XX			
DE	Human polypeptide SEQ ID NO 27222.		
XX			
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;		
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;		
KW	tissue growth factor; immunomodulatory; cancer; leukaemia;		
KW	nervous system disorders; arthritis; inflammation.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200164835-A2.		
XX			
PD	07-SEP-2001.		
XX			
PF	26-FEB-2001; 2001WO-US04927.		
XX			
PR	28-FEB-2000; 2000US-0515126.		
PR	18-MAY-2000; 2000US-0577409.		
XX			
PA	(HYSE-) HYSEQ INC.		
XX			
PI	Tang YT, Liu C, Dirmanac RT;		
XX			
DR	WPI: 2001-514838/56.		
DR	N-PSDB; AAI93261.		
XX			
PT	Isolated nucleic acids and polypeptides, useful for preventing		
PT	diagnosing and treating e.g. leukaemia, inflammation and immune		
PT	disorders -		
XX			
XX	Claim 20; SEQ ID NO 27222; 1399pp + Sequence Listing; English.		
XX			
XX	The invention relates to human polynucleotides (AAI79941-AAI93841) and		
CC	the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to		
CC	cytokine, cell proliferation or cell differentiation or which may induce		
CC	production of other cytokines in other cell populations. The		
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or		
CC	peptide therapy. The polypeptides have various cytokine-like activities,		
CC	e.g. stem cell growth factor activity, haematopoiesis regulating		
CC	activity, tissue growth factor activity, immunomodulatory activity and		
CC	activin/inhibin activity and may be useful in the diagnosis and/or		
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and		
CC	inflammation.		
CC	Note: The sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format directly from WIPO		
CC	at ftp.wipo.int/pub/published_pct_sequences.		
XX			
XX	Sequence 42 AA;		
XX			

```

Query Match      2.44; Score 8; DB 22; Length 42;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      244 SLANVVKP 251
      |||||
Db      32 slnmvxp 39

RESULT 12
AAO13438
ID      AAO13438 standard; Protein; 44 AA.
IX

```

AC AAO13438;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 27330.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
XX
PT 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-514838/56.
XX
DR N-PSDB: AA193369.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 27330; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 44 AA;
OY 244 SLANWKP 251
DB 34 slannwkp 41
RESULT 13
ABG05119
ID ABG05119 standard; Protein: 45 AA.
XX
AC ABG05119;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #5110.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PT 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
XX
DR N-PSDB: AA569306.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID NO 35478; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 45 AA;
OY 244 SLANWKP 251
DB 35 slannwkp 42
RESULT 14
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XX
AC AAO13238;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 27130.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
XX 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
XX N-PSDB; AAI93169.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing,
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 27130; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 45 AA;

Query Match 2.4%; Score 8; DB 22; Length 45;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 244 SLANWKP 251
DB 34 slanwkp 41

RESULT 15
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XX
AC AAO02012;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 15904.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200164835-A2.
XX

PD 07-SEP-2001.
XX
PF 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
XX 18-MAY-2000; 2000US-0577409.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-514838/56.
XX N-PSDB; AAI81943.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 15904; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
CC the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 46 AA;

Query Match 2.4%; Score 8; DB 22; Length 46;
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 39 slanwkp 46

Search completed: September 25, 2002, 09:52:39
Job time: 178 sec

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OM protein - protein search, using sw model

Run on: September 25, 2002, 09:50:06 ; Search time 13.2 Seconds
(without alignments)
606,939 Million cell updates/sec

Title: US-09-184-826-2

Perfect score: 328

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued_Patents_AA.*

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- 4: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/1aa/Backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	9	2.7	622	4	US-09-075-272-2
5	8	2.4	441	4	US-09-172-045-2
6	8	2.4	1015	2	US-08-374-483-4
7	8	2.4	1015	2	US-08-374-483-7
8	2	2.1	267	4	US-08-818-112-142
9	2	2.1	267	4	US-08-818-111-137
10	7	2.1	267	4	US-09-056-556-142
11	7	2.1	339	2	US-08-892-880-3
12	7	2.1	339	2	US-07-946-497-7
13	7	2.1	339	2	US-08-483-322-7
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15	7	2.1	503	1	US-07-946-497-2
16	7	2.1	503	1	US-08-483-322-2
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18	7	2.1	503	1	US-08-483-322-2
19	7	2.1	717	4	US-08-910-925-1
20	7	2.1	743	4	US-08-910-925-3
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25	6	1.8	13	2	US-08-651-818A-6
26	6	1.8	13	2	US-09-184-826-6
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114	6	1.8	275	4	US-09-230-180-16	Sequence 16, Appl	187	6	1.8	508	4	US-08-484-105-24	Sequence 24, Appl
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117	6	1.8	314	2	US-08-989-478-5	Sequence 5, Appl1	190	6	1.8	508	2	US-09-005-332A-2	Sequence 2, Appl1
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120	6	1.8	327	2	US-08-651-818A-3	Sequence 3, Appl1	193	6	1.8	508	1	US-08-467-852A-3	Sequence 3, Appl1
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141	6	1.8	376	1	US-08-081-328-4	Sequence 4, Appl1	214	6	1.8	508	1	US-08-127-499A-23	Sequence 23, Appl
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155	6	1.8	427	4	US-08-154-712B-15	Sequence 15, Appl	228	6	1.8	508	2	PCT-US93-11725-4	Sequence 4, Appl1
156	6	1.8	447	1	US-08-844-010-2	Sequence 2, Appl1	229	6	1.8	508	2	PCT-US96-10893-3	Sequence 3, Appl1
157	6	1.8	447	3	US-09-012-873-2	Sequence 2, Appl1	230	6	1.8	508	2	PCT-US93-11725-2	Sequence 2, Appl1
158	6	1.8	457	3	US-09-142-759-1	Sequence 1, Appl1	231	6	1.8	508	4	US-08-460-269C-4	Sequence 4, Appl1
159	6	1.8	462	3	US-08-484-438-42	Sequence 42, Appl	232	6	1.8	508	2	US-08-460-269C-6	Sequence 6, Appl1
160	6	1.8	462	3	US-08-875-944B-5	Sequence 5, Appl1	233	6	1.8	508	3	US-09-283-763-2	Sequence 3, Appl1
161	6	1.8	462	4	US-09-116-049-4	Sequence 4, Appl1	234	6	1.8	508	1	US-08-162-809-2	Sequence 2, Appl1
162	6	1.8	466	2	US-08-836-791-9	Sequence 9, Appl1	235	6	1.8	508	1	PCT-US93-11725-4	Sequence 4, Appl1
163	6	1.8	472	4	US-09-088-425-1	Sequence 1, Appl1	236	6	1.8	508	2	US-08-673-789-6	Sequence 6, Appl1
164	6	1.8	495	6	5516630-4	Patent No. 5516630	237	6	1.8	508	3	US-08-331-625A-52	Sequence 52, Appl
165	6	1.8	502	1	US-08-496-855A-4	Sequence 4, Appl1	238	6	1.8	508	3	US-08-331-625A-54	Sequence 54, Appl
166	6	1.8	502	2	US-08-466-589-10	Sequence 10, Appl	239	6	1.8	508	3	US-09-098-601-2	Sequence 2, Appl1
167	6	1.8	502	2	US-08-700-636-10	Sequence 10, Appl	240	6	1.8	508	3	US-09-220-641-3	Sequence 3, Appl1
168	6	1.8	502	3	US-08-467-574-10	Sequence 10, Appl	241	6	1.8	508	4	US-09-540-245A-17	Sequence 17, Appl
169	6	1.8	502	4	US-09-217-345-10	Sequence 10, Appl	242	6	1.8	508	4	US-09-357-251-37	Sequence 37, Appl
170	6	1.8	508	1	US-08-472-028A-4	Sequence 4, Appl1	243	6	1.8	508	4	US-08-308-872B-2	Sequence 2, Appl1
171	6	1.8	508	3	US-08-808-931-4	Sequence 4, Appl1	244	6	1.8	508	6	US-08-308-872B-4	Sequence 4, Appl1
172	6	1.8	508	3	US-08-808-323-4	Sequence 4, Appl1	245	6	1.8	508	6	US-08-331-625A-2	Sequence 2, Appl1
173	6	1.8	508	3	US-09-050-603A-4	Sequence 4, Appl1	246	6	1.8	508	5	PCT-US93-04384-18	Sequence 18, Appl

247	6	1.8	1452	5	PCT-US93-04692-2	Sequence 2, Appli	320	5	1.5	12	1	US-08-467-607-6	Sequence 6, Appli
248	6	1.8	1453	4	US-08-308-872B-6	Sequence 22, Appli	321	5	1.5	12	2	US-08-467-607-8	Sequence 8, Appli
249	6	1.8	1454	1	US-08-392-459-22	Sequence 6, Appli	322	5	1.5	12	2	US-08-469-362-6	Sequence 6, Appli
250	6	1.8	1454	4	US-08-392-459-26	Sequence 26, Appli	323	5	1.5	12	2	US-08-469-362-8	Sequence 8, Appli
251	6	1.8	1454	4	US-08-392-459-32	Sequence 32, Appli	324	5	1.5	12	2	US-08-850-392-6	Sequence 6, Appli
252	6	1.8	1454	5	PCT-US91-08525-22	Sequence 22, Appli	325	5	1.5	12	2	US-08-850-392-8	Sequence 8, Appli
253	6	1.8	1454	5	PCT-US91-08525-26	Sequence 26, Appli	326	5	1.5	12	2	PCT-US95-05471-10	Sequence 10, Appli
254	6	1.8	1454	5	PCT-US91-08525-32	Sequence 32, Appli	327	5	1.5	12	2	US-08-769-745-30	Sequence 30, Appli
255	6	1.8	1454	5	PCT-US93-04384-2	Sequence 2, Appli1	328	5	1.5	13	3	US-08-648-332-9	Sequence 9, Appli1
256	6	1.8	1454	5	PCT-US93-04384-8	Sequence 8, Appli1	329	5	1.5	14	1	US-08-279-754-5	Sequence 5, Appli1
257	6	1.8	1454	5	PCT-US93-04384-12	Sequence 12, Appli	330	5	1.5	14	1	US-08-484-969-1	Sequence 1, Appli1
258	6	1.8	1454	5	PCT-US93-04384-16	Sequence 16, Appli	331	5	1.5	14	1	US-08-484-969-2	Sequence 2, Appli1
259	6	1.8	1454	5	PCT-US93-04384-43	Sequence 43, Appli	332	5	1.5	14	1	US-08-472-627-1	Sequence 1, Appli1
260	6	1.8	1454	5	PCT-US93-04384-44	Sequence 44, Appli	333	5	1.5	14	1	US-08-472-627-2	Sequence 2, Appli1
261	6	1.8	1454	5	PCT-US93-04384-45	Sequence 45, Appli	334	5	1.5	14	1	US-08-388-463-1	Sequence 1, Appli1
262	6	1.8	1454	5	PCT-US93-04384-46	Sequence 46, Appli	335	5	1.5	14	1	US-08-388-463-2	Sequence 2, Appli1
263	6	1.8	1454	5	PCT-US93-04384-47	Sequence 47, Appli	336	5	1.5	14	1	US-08-188-277B-20	Sequence 20, Appli
264	6	1.8	1454	5	PCT-US93-04384-48	Sequence 48, Appli	337	5	1.5	14	2	US-08-424-268-22	Sequence 22, Appli
265	6	1.8	1481	4	US-09-251-645-14	Sequence 14, Appli	338	5	1.5	14	2	US-09-458-483B-16	Sequence 16, Appli
266	6	1.8	1579	3	US-08-755-587-184	Sequence 184, App	339	5	1.5	14	4	PCT-US93-10442-22	Sequence 22, Appli
267	6	1.8	1612	3	US-08-545-860D-48	Sequence 48, Appli	340	5	1.5	14	5	PCT-US95-09052-5	Sequence 5, Appli1
268	6	1.8	1612	5	PCT-US94-04496-18	Sequence 48, Appli	341	5	1.5	15	1	US-08-116-733-2	Sequence 2, Appli1
269	6	1.8	1782	2	US-08-962-284-2	Sequence 2, Appli	342	5	1.5	15	1	US-08-190-802A-17	Sequence 17, Appli
270	6	1.8	1782	2	US-08-962-284-4	Sequence 4, Appli1	343	5	1.5	15	1	US-08-218-025A-159	Sequence 159, App
271	6	1.8	2227	3	US-08-475-886-2	Sequence 2, Appli1	344	5	1.5	15	1	US-08-469-615-1	Sequence 1, Appli1
272	6	1.8	2227	3	US-08-475-886-4	Sequence 4, Appli1	345	5	1.5	15	1	US-08-208-181A-19	Sequence 19, Appli
273	6	1.8	2227	3	US-08-475-886-6	Sequence 6, Appli1	346	5	1.5	15	1	US-08-466-763-1	Sequence 1, Appli1
274	6	1.8	2227	4	US-08-397-232-2	Sequence 2, Appli1	347	5	1.5	15	2	US-08-687-956A-3	Sequence 3, Appli1
275	6	1.8	2227	4	US-08-397-232-4	Sequence 4, Appli1	348	5	1.5	15	2	US-08-687-956A-6	Sequence 6, Appli1
276	6	1.8	2329	4	US-09-171-387-2	Sequence 2, Appli1	349	5	1.5	15	2	US-08-432-871C-81	Sequence 81, Appli
277	6	1.8	2329	4	US-08-755-587-16	Sequence 16, Appli	350	5	1.5	15	2	US-08-411-142A-1	Sequence 1, Appli1
278	6	1.8	2516	3	US-08-374-077C-2	Sequence 2, Appli1	351	5	1.5	15	4	US-08-477-346-17	Sequence 17, Appli
279	6	1.8	2516	4	US-08-895-590-2	Sequence 2, Appli1	352	5	1.5	15	4	US-08-743-168B-23	Sequence 23, Appli
280	6	1.8	3031	1	US-07-689-008-2	Sequence 2, Appli1	353	5	1.5	15	4	US-09-230-548-23	Sequence 23, Appli
281	6	1.8	3418	2	US-08-639-501-2	Sequence 2, Appli1	354	5	1.5	15	4	US-08-473-089-17	Sequence 17, Appli
282	6	1.8	3418	2	US-08-603-753D-4	Sequence 2, Appli1	355	5	1.5	15	5	PCT-US96-10435-23	Sequence 23, Appli
283	6	1.8	3418	3	US-09-044-946-2	Sequence 2, Appli1	356	5	1.5	16	1	US-08-188-277B-27	Sequence 27, Appli
284	6	1.8	3418	3	US-08-755-587-44	Sequence 44, Appli	357	5	1.5	16	2	US-08-849-536A-8	Sequence 8, Appli1
285	6	1.8	3418	3	US-09-044-946-2	Sequence 2, Appli1	358	5	1.5	16	2	US-08-574-959A-16	Sequence 16, Appli
286	6	1.8	3418	4	US-09-099-753-4	Sequence 4, Appli1	359	5	1.5	17	1	US-09-357-014-16	Sequence 4, Appli1
287	6	1.8	3418	4	US-08-986-106-4	Sequence 4, Appli1	360	5	1.5	17	1	US-08-304-585-4	Sequence 4, Appli1
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289	6	1.8	4613	4	US-09-105-537-31	Sequence 31, Appli	362	5	1.5	17	2	US-08-726-306A-112	Sequence 112, App
290	6	1.8	11877	4	US-09-105-537-6	Sequence 6, Appli1	363	5	1.5	17	2	US-08-574-959A-15	Sequence 15, Appli
291	5	1.5	5	1	US-07-969-305-17	Sequence 17, Appli	364	5	1.5	17	3	US-09-136-218-16	Sequence 16, Appli
292	5	1.5	5	2	US-08-651-818A-10	Sequence 10, Appli	365	5	1.5	17	4	US-08-602-999A-413	Sequence 413, App
293	5	1.5	5	2	US-09-184-826-10	Sequence 10, Appli	366	5	1.5	17	4	US-09-357-014-15	Sequence 15, Appli
294	5	1.5	7	4	US-09-139-802-142	Sequence 142, App	367	5	1.5	18	1	US-08-205-938A-22	Sequence 22, Appli
295	5	1.5	8	1	US-08-290-301-74	Sequence 74, Appli	368	5	1.5	18	3	US-08-940-095-226	Sequence 226, App
296	5	1.5	9	1	US-08-302-808-9	Sequence 9, Appli1	369	5	1.5	18	3	US-08-940-093-226	Sequence 226, App
297	5	1.5	9	2	US-08-986-948-9	Sequence 9, Appli1	370	5	1.5	18	3	US-08-940-096-326	Sequence 326, App
298	5	1.5	9	4	US-08-704-344-10	Sequence 10, Appli	371	5	1.5	18	4	US-09-465-719-226	Sequence 226, App
299	5	1.5	9	4	US-09-492-543-73	Sequence 73, Appli	372	5	1.5	18	4	US-09-453-605-226	Sequence 226, App
300	5	1.5	9	4	US-09-492-543-101	Sequence 101, App	373	5	1.5	18	5	PCT-US95-02662-22	Sequence 22, Appli
301	5	1.5	9	4	PCT-US95-16415-19	Sequence 19, Appli	374	5	1.5	19	5	US-07-598-489B-1	Sequence 1, Appli1
302	5	1.5	10	2	US-07-885-089B-27	Sequence 27, Appli	375	5	1.5	19	2	US-08-031-538-42	Sequence 42, Appli
303	5	1.5	10	2	US-08-538-711A-5	Sequence 5, Appli1	376	5	1.5	19	5	PCT-US91-02227-1	Sequence 1, Appli1
304	5	1.5	10	3	US-08-339-141A-2	Sequence 2, Appli1	377	5	1.5	20	1	US-08-218-025A-91	Sequence 91, Appli
305	5	1.5	10	4	US-08-836-075A-176	Sequence 176, App	378	5	1.5	20	2	US-08-726-306A-24	Sequence 24, Appli
306	5	1.5	10	4	US-08-725-027-5	Sequence 5, Appli1	379	5	1.5	20	3	US-08-658-857B-16	Sequence 16, Appli
307	5	1.5	10	5	PCT-US95-14659-2	Sequence 2, Appli1	380	5	1.5	20	3	US-08-763-226C-16	Sequence 16, Appli
308	5	1.5	11	1	US-08-338-634-8	Sequence 8, Appli1	381	5	1.5	20	3	US-08-467-023-31	Sequence 31, Appli
309	5	1.5	11	2	US-08-676-279-1	Sequence 1, Appli1	382	5	1.5	20	3	US-08-467-023-32	Sequence 32, Appli
310	5	1.5	11	2	US-08-676-279-2	Sequence 2, Appli1	383	5	1.5	20	4	US-09-162-934-13	Sequence 13, Appli
311	5	1.5	11	2	US-08-982-597A-11	Sequence 11, Appli	384	5	1.5	20	4	US-09-307-200-16	Sequence 16, Appli
312	5	1.5	11	2	US-08-310-912A-114	Sequence 114, App	385	5	1.5	20	6	5262298-2	Patent No. 5262298
313	5	1.5	11	4	US-09-136-218-11	Sequence 11, App	386	5	1.5	20	6	5262298-4	Patent No. 5262298
314	5	1.5	11	4	US-09-301-085-114	Sequence 114, App	387	5	1.5	21	2	US-08-031-538-45	Sequence 45, Appli
315	5	1.5	11	5	PCT-US92-03432-8	Sequence 8, Appli1	388	5	1.5	22	3	US-08-476-509B-10	Sequence 10, Appli
316	5	1.5	11	5	PCT-US92-03432-16	Sequence 16, Appli	389	5	1.5	23	1	US-07-946-497-8	Sequence 8, Appli1
317	5	1.5	11	5	PCT-US95-04589-114	Sequence 114, App	390	5	1.5	23	1	US-08-483-323-8	Sequence 8, Appli1
318	5	1.5	11	5	PCT-US95-16415-18	Sequence 18, Appli	391	5	1.5	23	2	US-08-478-883-8	Sequence 8, Appli1
319	5	1.5	12	1	US-08-260-582-10	Sequence 10, Appli	392	5	1.5	23	2	US-08-727-688-31	Sequence 31, Appli

393	5	1.5	23	3	US-09-045-632-59	Sequence 59, Appl	466	5	1.5	35	1	US-08-205-938A-39	Sequence 39, Appl
394	5	1.5	24	1	US-08-371-990-8	Sequence 8, Appl1	467	5	1.5	35	1	US-08-475-989-3	Sequence 3, Appl1
395	5	1.5	24	1	PCT-US94-01712-8	Sequence 8, Appl1	468	5	1.5	35	2	US-08-612-785B-15	Sequence 15, Appl
396	5	1.5	25	2	US-08-457-192-1	Sequence 1, Appl1	469	5	1.5	35	2	US-08-612-785B-16	Sequence 16, Appl
397	5	1.5	25	2	US-08-528-057-16	Sequence 16, Appl	470	5	1.5	35	2	US-08-612-785B-36	Sequence 36, Appl
398	5	1.5	25	2	US-08-528-057-30	Sequence 30, Appl	471	5	1.5	35	2	US-08-612-785B-38	Sequence 38, Appl
399	5	1.5	26	1	US-07-942-245-360	Sequence 360, App	472	5	1.5	35	2	US-08-612-785B-39	Sequence 39, Appl
400	5	1.5	26	1	US-07-942-245-438	Sequence 438, App	473	5	1.5	35	2	US-08-612-785B-40	Sequence 40, Appl
401	5	1.5	26	6	5262298-3	Patent No. 5262298	474	5	1.5	35	2	US-08-766-858A-41	Sequence 41, Appl
402	5	1.5	27	2	US-08-557-309B-46	Sequence 46, Appl	475	5	1.5	35	2	US-08-475-985-3	Sequence 3, Appl1
403	5	1.5	27	3	US-08-834-306-46	Sequence 46, Appl	476	5	1.5	35	2	US-08-472-721-15	Sequence 15, Appl
404	5	1.5	27	3	US-09-093-227-24	Sequence 24, Appl	477	5	1.5	35	3	US-08-266-839-3	Sequence 3, Appl1
405	5	1.5	27	4	US-08-993-674A-46	Sequence 46, Appl	478	5	1.5	35	4	US-08-266-839-3	Sequence 3, Appl1
406	5	1.5	28	1	US-08-427-072-9	Sequence 9, Appl1	479	5	1.5	35	4	US-09-001-984C-11	Sequence 11, Appl
407	5	1.5	28	3	US-08-788-231A-18	Sequence 18, Appl	480	5	1.5	35	4	US-09-001-984C-42	Sequence 42, Appl
408	5	1.5	29	1	US-08-188-582-33	Sequence 33, Appl	481	5	1.5	35	4	US-08-617-267C-15	Sequence 15, Appl
409	5	1.5	29	1	US-08-646-715-33	Sequence 33, Appl	482	5	1.5	35	5	US-08-617-267C-16	Sequence 16, Appl
410	5	1.5	29	3	US-08-399-561-3	Sequence 3, Appl1	483	5	1.5	35	5	PCT-US95-02626-33	Sequence 33, Appl
411	5	1.5	29	3	US-08-648-322-7	Sequence 7, Appl1	484	5	1.5	35	5	PCT-US95-02626-35	Sequence 35, Appl
412	5	1.5	30	1	US-07-596-081A-33	Sequence 33, Appl	485	5	1.5	35	5	PCT-US95-02626-37	Sequence 37, Appl
413	5	1.5	30	1	US-08-185-424B-5	Sequence 5, Appl1	486	5	1.5	36	1	US-08-240-012-3	Sequence 3, Appl1
414	5	1.5	30	2	US-08-553-501A-76	Sequence 76, Appl	487	5	1.5	36	2	US-08-746-283-22	Sequence 22, Appl
415	5	1.5	30	2	US-08-553-501A-80	Sequence 80, Appl	488	5	1.5	36	2	US-08-602-264A-9	Sequence 9, Appl1
416	5	1.5	30	2	US-08-716-317-16	Sequence 16, Appl	489	5	1.5	36	2	US-08-746-257A-20	Sequence 20, Appl
417	5	1.5	30	3	US-09-205-231-76	Sequence 76, Appl	490	5	1.5	36	3	US-08-856-074A-32	Sequence 32, Appl
418	5	1.5	30	3	US-09-205-231-80	Sequence 80, Appl	491	5	1.5	36	3	US-08-856-074A-32	Sequence 32, Appl
419	5	1.5	31	1	US-08-190-802A-73	Sequence 73, Appl	492	5	1.5	36	3	US-08-461-018A-6	Sequence 6, Appl1
420	5	1.5	31	1	US-08-190-802A-104	Sequence 104, App	493	5	1.5	36	4	US-08-896-162A-3	Sequence 3, Appl1
421	5	1.5	31	1	US-08-190-802A-132	Sequence 132, App	494	5	1.5	36	4	US-08-896-162A-3	Sequence 3, Appl1
422	5	1.5	31	1	US-08-190-802A-160	Sequence 160, App	495	5	1.5	37	4	US-09-216-958-9	Sequence 9, Appl1
423	5	1.5	31	1	US-08-190-802A-176	Sequence 176, App	496	5	1.5	37	4	US-08-836-252A-4	Sequence 4, Appl1
424	5	1.5	31	1	US-08-190-802A-244	Sequence 244, App	497	5	1.5	38	1	US-09-488-799-77	Sequence 77, Appl
425	5	1.5	31	1	US-08-179-632-2	Sequence 2, Appl1	498	5	1.5	38	1	US-08-179-632-7	Sequence 7, Appl
426	5	1.5	31	1	US-08-440-174A-2	Sequence 2, Appl1	499	5	1.5	38	1	US-08-440-174A-7	Sequence 7, Appl1
427	5	1.5	31	2	US-08-105-989-19	Sequence 19, Appl	500	5	1.5	38	1	US-08-403-378B-5	Sequence 5, Appl1
428	5	1.5	31	2	US-08-105-989-24	Sequence 24, Appl	501	5	1.5	38	2	US-08-622-753A-6	Sequence 6, Appl1
429	5	1.5	31	3	US-08-793-937-3	Sequence 3, Appl1	502	5	1.5	38	5	PCT-US95-00062-7	Sequence 7, Appl1
430	5	1.5	31	3	US-08-856-074A-33	Sequence 33, Appl	503	5	1.5	39	4	US-08-346-147B-42	Sequence 42, Appl
431	5	1.5	31	4	US-09-138-922-19	Sequence 19, Appl	504	5	1.5	39	5	PCT-US96-01735-2	Sequence 2, Appl1
432	5	1.5	31	4	US-09-138-922-24	Sequence 24, Appl	505	5	1.5	40	1	US-07-744-767A-1	Sequence 1, Appl1
433	5	1.5	31	4	US-09-235-283-3	Sequence 3, Appl1	506	5	1.5	40	1	US-08-235-400-2	Sequence 2, Appl1
434	5	1.5	31	4	US-08-477-346-73	Sequence 73, Appl	507	5	1.5	40	1	US-08-179-632-3	Sequence 3, Appl1
435	5	1.5	31	4	US-08-477-346-104	Sequence 104, App	508	5	1.5	40	1	US-08-179-632-4	Sequence 4, Appl1
436	5	1.5	31	4	US-08-477-346-132	Sequence 132, App	509	5	1.5	40	1	US-08-179-632-5	Sequence 5, Appl1
437	5	1.5	31	4	US-08-477-346-160	Sequence 160, App	510	5	1.5	40	1	US-08-476-464A-2	Sequence 2, Appl1
438	5	1.5	31	4	US-08-477-346-176	Sequence 176, App	511	5	1.5	40	1	US-08-440-174A-3	Sequence 3, Appl1
439	5	1.5	31	4	US-08-477-346-244	Sequence 244, App	512	5	1.5	40	1	US-08-440-174A-4	Sequence 4, Appl1
440	5	1.5	31	4	US-08-477-346-244	Sequence 244, App	513	5	1.5	40	1	US-08-440-174A-5	Sequence 5, Appl1
441	5	1.5	31	4	US-08-473-089-73	Sequence 73, Appl	514	5	1.5	40	1	US-08-304-585-1	Sequence 1, Appl1
442	5	1.5	31	4	US-08-473-089-104	Sequence 104, App	515	5	1.5	40	1	US-08-304-585-8	Sequence 8, Appl1
443	5	1.5	31	4	US-08-473-089-132	Sequence 132, App	516	5	1.5	40	1	US-08-302-808-3	Sequence 3, Appl1
444	5	1.5	31	4	US-08-473-089-160	Sequence 160, App	517	5	1.5	40	2	US-08-433-734-1	Sequence 1, Appl1
445	5	1.5	31	4	US-08-473-089-176	Sequence 176, App	518	5	1.5	40	2	US-08-609-090-8	Sequence 8, Appl1
446	5	1.5	31	4	US-08-473-089-244	Sequence 244, App	519	5	1.5	40	2	US-08-609-090-8	Sequence 8, Appl1
447	5	1.5	31	5	PCT-US95-00062-2	Sequence 2, Appl1	520	5	1.5	40	2	US-07-737-371E-69	Sequence 69, Appl
448	5	1.5	32	1	US-07-596-081A-12	Sequence 12, Appl	521	5	1.5	40	2	US-08-682-248A-2	Sequence 2, Appl1
449	5	1.5	32	1	US-08-179-632-1	Sequence 1, Appl1	522	5	1.5	40	2	US-08-986-948-3	Sequence 3, Appl1
450	5	1.5	32	2	US-08-440-174A-1	Sequence 21, Appl	523	5	1.5	40	2	US-08-461-216-1	Sequence 1, Appl1
451	5	1.5	32	2	US-08-716-317-21	Sequence 21, Appl	524	5	1.5	40	4	US-08-959-148-1	Sequence 1, Appl1
452	5	1.5	32	3	US-08-954-915A-29	Sequence 29, Appl	525	5	1.5	40	4	US-09-242-724-22	Sequence 22, Appl
453	5	1.5	32	5	PCT-US95-00062-1	Sequence 1, Appl1	526	5	1.5	40	5	US-08-723-661B-1	Sequence 1, Appl1
454	5	1.5	33	6	5432076-1	Patent No. 5432076	527	5	1.5	40	5	PCT-US92-06700-1	Sequence 1, Appl1
455	5	1.5	33	2	US-08-237-716-11	Sequence 11, Appl	528	5	1.5	40	5	PCT-US95-00062-3	Sequence 3, Appl1
456	5	1.5	33	4	US-08-376-843-49	Sequence 49, Appl	529	5	1.5	40	5	PCT-US95-00062-4	Sequence 4, Appl1
457	5	1.5	34	1	US-08-836-252A-1	Sequence 1, Appl1	530	5	1.5	40	5	PCT-US95-00062-5	Sequence 5, Appl1
458	5	1.5	34	1	US-08-085-122-11	Sequence 11, Appl1	531	5	1.5	41	1	US-07-819-361-1	Sequence 1, Appl1
459	5	1.5	34	2	US-08-528-057-15	Sequence 15, Appl	532	5	1.5	41	1	US-08-170-632-8	Sequence 8, Appl1
460	5	1.5	34	2	US-08-475-579A-4	Sequence 4, Appl1	533	5	1.5	41	1	US-08-440-174A-8	Sequence 8, Appl1
461	5	1.5	34	2	US-08-319-052-21	Sequence 21, Appl	534	5	1.5	41	1	US-08-302-808-4	Sequence 4, Appl1
462	5	1.5	34	4	US-08-716-317-26	Sequence 26, Appl	535	5	1.5	41	2	US-08-682-245A-3	Sequence 3, Appl1
463	5	1.5	35	1	US-08-442-108B-21	Sequence 21, Appl	536	5	1.5	41	3	US-08-986-948-4	Sequence 3, Appl1
464	5	1.5	35	1	US-08-205-938A-33	Sequence 33, Appl	537	5	1.5	41	4	US-08-856-074A-11	Sequence 11, Appl
465	5	1.5	35	1	US-08-205-938A-35	Sequence 35, Appl	538	5	1.5	41	5	US-09-277-716-23	Sequence 23, Appl
					US-08-205-938A-37	Sequence 37, Appl						PCT-US95-00062-8	Sequence 8, Appl1

539	5	1.5	42	1	US-07-744-767A-2	Sequence 2, Appl1	612	5	1.5	43	4	US-09-390-692-1	Sequence 1, Appl1
540	5	1.5	42	1	US-08-179-574-1	Sequence 1, Appl1	613	5	1.5	43	4	US-08-617-267C-1	Sequence 1, Appl1
541	5	1.5	42	1	US-08-271-162-5	Sequence 5, Appl1	614	5	1.5	43	4	US-08-617-267C-3	Sequence 3, Appl1
542	5	1.5	42	1	US-08-347-144-1	Sequence 1, Appl1	615	5	1.5	43	4	US-09-303-655-1	Sequence 1, Appl1
543	5	1.5	42	1	US-08-462-859A-19	Sequence 19, Appl1	616	5	1.5	43	4	PCT-US93-12588-10	Sequence 10, Appl1
544	5	1.5	42	1	US-08-123-659A-19	Sequence 19, Appl1	617	5	1.5	43	5	PCT-US93-12588-69	Sequence 69, Appl1
545	5	1.5	42	1	US-08-464-247A-19	Sequence 19, Appl1	618	5	1.5	43	5	PCT-US95-00062-6	Sequence 6, Appl1
546	5	1.5	42	1	US-08-464-248A-19	Sequence 19, Appl1	619	5	1.5	43	5	PCT-US95-08071-10	Sequence 10, Appl1
547	5	1.5	42	1	US-08-476-464A-1	Sequence 1, Appl1	620	5	1.5	43	5	PCT-US95-08071-69	Sequence 69, Appl1
548	5	1.5	42	1	US-08-304-585-2	Sequence 2, Appl1	621	5	1.5	43	5	PCT-US95-14659-1	Sequence 1, Appl1
549	5	1.5	42	1	US-08-302-808-5	Sequence 5, Appl1	622	5	1.5	43	6	5187153-12	Patent No. 5187153
550	5	1.5	42	1	US-08-268-348A-1	Sequence 1, Appl1	623	5	1.5	44	4	US-08-687-590-21	Sequence 21, Appl1
551	5	1.5	42	1	US-08-268-348A-2	Sequence 2, Appl1	624	5	1.5	44	4	US-08-687-590-22	Sequence 22, Appl1
552	5	1.5	42	1	US-08-268-348A-3	Sequence 3, Appl1	625	5	1.5	44	4	US-08-687-590-23	Sequence 23, Appl1
553	5	1.5	42	1	US-08-268-348A-4	Sequence 4, Appl1	626	5	1.5	44	4	US-08-687-590-25	Sequence 5, Appl1
554	5	1.5	42	1	US-08-268-348A-5	Sequence 5, Appl1	627	5	1.5	45	1	US-08-123-659A-5	Sequence 5, Appl1
555	5	1.5	42	2	US-08-433-734-2	Sequence 2, Appl1	628	5	1.5	45	1	US-08-464-247A-5	Sequence 5, Appl1
556	5	1.5	42	2	US-08-609-090-9	Sequence 9, Appl1	629	5	1.5	45	1	US-08-464-248A-5	Sequence 5, Appl1
557	5	1.5	42	2	US-07-737-371E-72	Sequence 72, Appl1	630	5	1.5	45	2	US-08-676-279-56	Sequence 56, Appl1
558	5	1.5	42	2	US-08-422-333-3	Sequence 3, Appl1	631	5	1.5	46	3	US-08-856-074A-30	Sequence 30, Appl1
559	5	1.5	42	2	US-08-682-245A-4	Sequence 4, Appl1	632	5	1.5	46	3	US-08-856-074A-39	Sequence 39, Appl1
560	5	1.5	42	2	US-08-986-948-5	Sequence 5, Appl1	633	5	1.5	47	2	US-08-609-090-10	Sequence 10, Appl1
561	5	1.5	42	3	US-08-717-551A-2	Sequence 2, Appl1	634	5	1.5	47	3	US-08-654-618-24	Sequence 24, Appl1
562	5	1.5	42	4	US-09-388-890-1	Sequence 1, Appl1	635	5	1.5	47	3	US-08-654-575-24	Sequence 24, Appl1
563	5	1.5	42	4	US-09-005-215-20	Sequence 20, Appl1	636	5	1.5	48	4	US-08-905-223-323	Sequence 23, Appl1
564	5	1.5	42	4	US-09-242-724-23	Sequence 23, Appl1	637	5	1.5	49	1	US-08-123-702-45	Sequence 45, Appl1
565	5	1.5	42	5	PCT-US92-06700-2	Sequence 2, Appl1	638	5	1.5	50	4	US-08-290-736C-11	Sequence 11, Appl1
566	5	1.5	42	5	PCT-US93-00325-1	Sequence 1, Appl1	639	5	1.5	52	1	US-08-340-428B-34	Sequence 34, Appl1
567	5	1.5	42	5	PCT-US95-08302-5	Sequence 5, Appl1	640	5	1.5	52	2	US-08-609-090-11	Sequence 11, Appl1
568	5	1.5	42	6	5220013-12	Patent No. 5220013	641	5	1.5	52	4	US-09-330-330-8	Sequence 8, Appl1
569	5	1.5	42	6	5220013-14	Patent No. 5220013	642	5	1.5	52	4	US-09-330-330-11	Sequence 11, Appl1
570	5	1.5	42	6	5223482-12	Patent No. 5223482	643	5	1.5	52	4	US-09-327-357-537	Sequence 537, Appl1
571	5	1.5	43	1	US-08-235-400-1	Sequence 1, Appl1	644	5	1.5	52	5	PCT-US93-07306-34	Sequence 34, Appl1
572	5	1.5	43	1	US-08-437-067-1	Sequence 1, Appl1	645	5	1.5	52	5	US-08-456-647B-16	Sequence 16, Appl1
573	5	1.5	43	1	US-08-179-632-6	Sequence 6, Appl1	646	5	1.5	53	2	US-08-456-647B-40	Sequence 40, Appl1
574	5	1.5	43	1	US-07-998-003A-10	Sequence 10, Appl1	647	5	1.5	53	2	US-08-237-401A-16	Sequence 16, Appl1
575	5	1.5	43	1	US-07-998-003A-69	Sequence 69, Appl1	648	5	1.5	53	2	US-08-237-401A-40	Sequence 40, Appl1
576	5	1.5	43	1	US-08-453-274B-10	Sequence 10, Appl1	649	5	1.5	53	4	US-09-173-887-5	Sequence 5, Appl1
577	5	1.5	43	1	US-08-453-274B-69	Sequence 69, Appl1	650	5	1.5	53	4	US-09-294-987-1	Sequence 1, Appl1
578	5	1.5	43	1	US-08-453-695A-10	Sequence 10, Appl1	651	5	1.5	54	4	US-09-227-357-212	Sequence 212, Appl1
579	5	1.5	43	1	US-08-453-695A-69	Sequence 69, Appl1	652	5	1.5	55	1	US-08-366-953A-39	Sequence 39, Appl1
580	5	1.5	43	1	US-08-440-174A-6	Sequence 6, Appl1	653	5	1.5	55	4	US-08-900-574-8	Sequence 8, Appl1
581	5	1.5	43	1	US-08-302-808-9	Sequence 9, Appl1	654	5	1.5	55	4	US-09-352-078-9	Sequence 9, Appl1
582	5	1.5	43	1	US-08-079-511-1	Sequence 1, Appl1	655	5	1.5	55	4	US-08-858-207A-511	Sequence 511, Appl1
583	5	1.5	43	1	US-08-467-607-1	Sequence 1, Appl1	656	5	1.5	57	4	US-09-015-030-11	Sequence 11, Appl1
584	5	1.5	43	1	US-08-268-161A-10	Sequence 10, Appl1	657	5	1.5	58	1	US-08-542-363-29	Sequence 29, Appl1
585	5	1.5	43	1	US-08-268-161A-69	Sequence 69, Appl1	658	5	1.5	58	4	US-09-100-089-29	Sequence 29, Appl1
586	5	1.5	43	2	US-08-404-831-1	Sequence 1, Appl1	659	5	1.5	59	1	US-08-484-963-3	Sequence 3, Appl1
587	5	1.5	43	2	US-08-404-831-3	Sequence 3, Appl1	660	5	1.5	59	1	US-08-472-627-3	Sequence 3, Appl1
588	5	1.5	43	2	US-08-602-264A-3	Sequence 3, Appl1	661	5	1.5	59	1	US-08-388-463-3	Sequence 3, Appl1
589	5	1.5	43	2	US-08-469-362-1	Sequence 1, Appl1	662	5	1.5	59	2	US-08-733-505A-55	Sequence 55, Appl1
590	5	1.5	43	2	US-08-612-785B-1	Sequence 1, Appl1	663	5	1.5	59	2	US-08-733-505A-56	Sequence 56, Appl1
591	5	1.5	43	2	US-08-612-785B-3	Sequence 3, Appl1	664	5	1.5	59	2	US-08-733-505A-57	Sequence 57, Appl1
592	5	1.5	43	2	US-08-475-579A-1	Sequence 1, Appl1	665	5	1.5	59	2	US-08-733-505A-58	Sequence 58, Appl1
593	5	1.5	43	2	US-08-475-579A-3	Sequence 3, Appl1	666	5	1.5	59	2	US-08-716-317-2	Sequence 2, Appl1
594	5	1.5	43	2	US-08-850-392-1	Sequence 1, Appl1	667	5	1.5	60	2	US-08-484-397A-31	Sequence 31, Appl1
595	5	1.5	43	2	US-07-737-371E-70	Sequence 70, Appl1	668	5	1.5	60	3	US-08-856-074A-1	Sequence 1, Appl1
596	5	1.5	43	2	US-08-453-702A-10	Sequence 10, Appl1	669	5	1.5	60	3	US-08-467-023-62	Sequence 62, Appl1
597	5	1.5	43	2	US-08-453-702A-69	Sequence 69, Appl1	670	5	1.5	62	1	US-08-428-091-1	Sequence 1, Appl1
598	5	1.5	43	2	US-08-986-948-6	Sequence 6, Appl1	671	5	1.5	63	1	US-08-462-859A-3	Sequence 3, Appl1
599	5	1.5	43	2	US-08-975-977-1	Sequence 1, Appl1	672	5	1.5	63	1	US-08-462-859A-4	Sequence 4, Appl1
600	5	1.5	43	2	US-08-817-162A-1	Sequence 1, Appl1	673	5	1.5	63	1	US-08-123-659A-4	Sequence 4, Appl1
601	5	1.5	43	2	US-08-920-162A-1	Sequence 1, Appl1	674	5	1.5	63	1	US-08-123-659A-3	Sequence 3, Appl1
602	5	1.5	43	3	US-08-461-018A-3	Sequence 3, Appl1	675	5	1.5	63	1	US-08-464-247A-3	Sequence 3, Appl1
603	5	1.5	43	3	US-08-976-191-1	Sequence 1, Appl1	676	5	1.5	63	1	US-08-464-247A-4	Sequence 4, Appl1
604	5	1.5	43	3	US-08-339-141A-1	Sequence 1, Appl1	677	5	1.5	63	1	US-08-464-248A-3	Sequence 3, Appl1
605	5	1.5	43	3	US-08-976-179-1	Sequence 1, Appl1	678	5	1.5	63	1	US-08-464-248A-4	Sequence 4, Appl1
606	5	1.5	43	3	US-09-116-958-3	Sequence 3, Appl1	679	5	1.5	66	4	US-09-461-697-312	Sequence 312, Appl1
607	5	1.5	43	4	US-09-099-639-10	Sequence 10, Appl1	680	5	1.5	68	1	US-08-180-761B-3	Sequence 3, Appl1
608	5	1.5	43	4	US-09-099-639-69	Sequence 69, Appl1	681	5	1.5	69	2	US-08-726-306A-53	Sequence 53, Appl1
609	5	1.5	43	4	US-09-356-931-1	Sequence 1, Appl1	682	5	1.5	69	4	US-08-965-762-34	Sequence 34, Appl1
610	5	1.5	43	4	US-08-733-202-1	Sequence 1, Appl1	683	5	1.5	71	1	US-08-280-443-22	Sequence 22, Appl1
611	5	1.5	43	4	US-08-703-675C-1	Sequence 1, Appl1	684	5	1.5	71	1	US-08-457-459-22	Sequence 22, Appl1

685	5	1.5	71	1	US-08-555-678-22	Sequence 22, Appl	758	5	1.5	95	2	US-08-330-161-12	Sequence 12, Appl
686	5	1.5	71	4	US-09-025-151-25	Sequence 25, Appl	759	5	1.5	95	2	US-08-456-241-14	Sequence 14, Appl
687	5	1.5	71	4	US-09-314-268-131	Sequence 131, App	760	5	1.5	95	2	US-08-440-401-12	Sequence 12, Appl
688	5	1.5	71	5	PCT-US95-02275-22	Sequence 22, Appl	761	5	1.5	95	2	US-08-419-878B-12	Sequence 12, Appl
689	5	1.5	73	1	US-07-609-716-109	Sequence 109, App	762	5	1.5	95	2	US-08-631-328-24	Sequence 24, Appl
690	5	1.5	73	1	US-07-609-716-110	Sequence 110, App	763	5	1.5	95	2	US-08-455-524B-24	Sequence 24, Appl
691	5	1.5	73	1	US-08-370-225-12	Sequence 12, Appl	764	5	1.5	95	2	US-08-455-021B-24	Sequence 24, Appl
692	5	1.5	73	1	US-08-461-859-12	Sequence 12, Appl	765	5	1.5	95	2	US-08-455-021B-24	Sequence 24, Appl
693	5	1.5	73	4	US-08-475-411A-109	Sequence 109, App	766	5	1.5	95	3	PCT-US92-04295A-14	Sequence 14, Appl
694	5	1.5	73	4	US-08-475-411A-110	Sequence 110, App	767	5	1.5	96	3	US-08-729-416C-5	Sequence 5, Appl
695	5	1.5	73	4	US-08-478-029A-109	Sequence 109, App	768	5	1.5	97	3	US-07-609-917B-99	Sequence 99, Appl
696	5	1.5	73	4	US-08-478-029A-110	Sequence 110, App	769	5	1.5	97	3	US-08-816-977-27	Sequence 27, Appl
697	5	1.5	73	5	PCT-US93-10069-12	Sequence 12, App	770	5	1.5	97	4	US-08-475-411A-99	Sequence 99, Appl
698	5	1.5	74	3	US-08-615-232A-6	Sequence 6, Appl	771	5	1.5	97	4	US-08-478-029A-99	Sequence 99, Appl
699	5	1.5	74	3	US-08-470-323-6	Sequence 6, Appl	772	5	1.5	97	4	US-09-309-487-23	Sequence 23, Appl
700	5	1.5	75	1	US-09-450-072-70	Sequence 70, Appl	773	5	1.5	97	6	5187153-8	Patent No. 5187153
701	5	1.5	76	1	US-07-956-862A-1	Sequence 1, Appl	774	5	1.5	97	6	5220013-8	Patent No. 5220013
702	5	1.5	76	1	US-08-250-958-1	Sequence 1, Appl	775	5	1.5	97	6	5223482-8	Patent No. 5223482
703	5	1.5	76	1	US-08-235-659-1	Sequence 1, Appl	776	5	1.5	99	1	US-08-127-499A-35	Sequence 35, Appl
704	5	1.5	76	1	US-08-480-449-20	Sequence 20, Appl	777	5	1.5	99	1	US-08-482-847-35	Sequence 35, Appl
705	5	1.5	76	2	US-08-716-188-2	Sequence 2, Appl	778	5	1.5	99	1	US-08-347-492B-8	Sequence 8, Appl
706	5	1.5	76	2	US-08-716-188-3	Sequence 3, Appl	779	5	1.5	99	1	US-08-480-449-19	Sequence 19, Appl
707	5	1.5	76	2	US-08-660-542-20	Sequence 20, Appl	780	5	1.5	99	2	US-08-479-126B-5	Sequence 5, Appl
708	5	1.5	76	2	US-08-615-232A-5	Sequence 5, Appl	781	5	1.5	99	2	US-08-421-144A-5	Sequence 5, Appl
709	5	1.5	76	3	US-08-470-323-5	Sequence 5, Appl	782	5	1.5	99	2	US-08-726-830A-5	Sequence 5, Appl
710	5	1.5	76	4	US-08-479-603-20	Sequence 20, Appl	783	5	1.5	99	2	US-08-422-333-3	Sequence 3, Appl
711	5	1.5	77	1	US-08-347-492B-9	Sequence 9, Appl	784	5	1.5	99	2	US-08-660-542-19	Sequence 19, Appl
712	5	1.5	77	2	US-08-421-144A-6	Sequence 6, Appl	785	5	1.5	99	2	US-08-798-143-8	Sequence 8, Appl
713	5	1.5	77	2	US-08-798-143-9	Sequence 9, Appl	786	5	1.5	99	2	US-09-047-125-7	Sequence 7, Appl
714	5	1.5	77	4	US-09-246-500B-7	Sequence 7, Appl	787	5	1.5	99	3	US-07-927-391-24	Sequence 24, Appl
715	5	1.5	78	1	US-08-330-163-12	Sequence 12, Appl	788	5	1.5	99	3	US-08-995-156A-5	Sequence 5, Appl
716	5	1.5	78	1	US-08-482-111-12	Sequence 12, Appl	789	5	1.5	99	3	US-08-339-708A-6	Sequence 6, Appl
717	5	1.5	78	2	US-07-885-089B-32	Sequence 32, Appl	790	5	1.5	99	3	US-08-339-708A-6	Sequence 6, Appl
718	5	1.5	78	4	US-09-448-086C-6	Sequence 6, Appl	791	5	1.5	99	3	US-08-339-708A-8	Sequence 8, Appl
719	5	1.5	79	5	PCT-US95-00605-1	Sequence 1, Appl	792	5	1.5	99	3	US-09-044-856A-5	Sequence 5, Appl
720	5	1.5	79	2	US-07-885-089B-31	Sequence 31, Appl	793	5	1.5	99	3	US-07-736-335E-7	Sequence 7, Appl
721	5	1.5	80	1	US-08-377-687-49	Sequence 49, Appl	794	5	1.5	99	3	US-09-044-855A-5	Sequence 5, Appl
722	5	1.5	80	1	US-08-377-687-59	Sequence 59, Appl	795	5	1.5	99	4	US-09-133-521-5	Sequence 5, Appl
723	5	1.5	80	1	US-08-832-883-5	Sequence 5, Appl	796	5	1.5	99	4	US-08-679-493A-152	Sequence 152, App
724	5	1.5	80	2	US-08-777-192-49	Sequence 49, Appl	797	5	1.5	99	4	US-08-479-603-19	Sequence 19, Appl
725	5	1.5	80	2	US-08-777-192-59	Sequence 59, Appl	798	5	1.5	99	4	US-09-367-206-16	Sequence 16, Appl
726	5	1.5	80	3	US-08-832-877-5	Sequence 5, Appl	799	5	1.5	99	4	US-09-227-357-156	Sequence 156, App
727	5	1.5	80	3	US-08-894-017-5	Sequence 5, Appl	800	5	1.5	99	4	US-09-199-637A-208	Sequence 208, App
728	5	1.5	80	4	US-08-971-982-49	Sequence 49, Appl	801	5	1.5	99	5	PCT-US96-10087-5	Sequence 5, Appl
729	5	1.5	80	4	US-08-971-982-59	Sequence 59, Appl	802	5	1.5	99	6	5212073-2	Patent No. 5212073
730	5	1.5	80	4	US-09-103-489-20	Sequence 20, Appl	803	5	1.5	100	6	5187153-10	Patent No. 5187153
731	5	1.5	83	1	US-07-881-075-17	Sequence 17, Appl	804	5	1.5	100	6	5220013-10	Patent No. 5220013
732	5	1.5	83	1	US-08-120-827-17	Sequence 17, Appl	805	5	1.5	100	6	5223482-10	Patent No. 5223482
733	5	1.5	83	1	US-08-168-091A-31	Sequence 31, Appl	806	5	1.5	101	4	US-09-199-637A-77	Sequence 77, Appl
734	5	1.5	83	1	US-08-478-675-17	Sequence 17, Appl	807	5	1.5	102	2	US-08-840-683-12	Sequence 12, Appl
735	5	1.5	83	4	US-09-227-357-652	Sequence 652, App	808	5	1.5	102	2	US-08-555-722-12	Sequence 12, Appl
736	5	1.5	84	1	US-08-925-757B-9	Sequence 9, Appl	809	5	1.5	102	3	US-08-654-618-25	Sequence 25, Appl
737	5	1.5	84	2	US-08-031-538-67	Sequence 67, Appl	810	5	1.5	102	3	US-08-654-575-25	Sequence 25, Appl
738	5	1.5	85	1	US-08-428-091-4	Sequence 4, Appl	811	5	1.5	102	4	US-09-384-301-12	Sequence 12, Appl
739	5	1.5	85	3	US-08-648-322-6	Sequence 6, Appl	812	5	1.5	103	2	US-08-404-831-2	Sequence 2, Appl
740	5	1.5	85	4	US-08-936-165A-423	Sequence 423, App	813	5	1.5	103	2	US-08-612-785B-2	Sequence 2, Appl
741	5	1.5	86	2	US-08-858-767-36	Sequence 36, Appl	814	5	1.5	103	2	US-08-475-579A-2	Sequence 2, Appl
742	5	1.5	86	2	US-08-863-028-36	Sequence 36, Appl	815	5	1.5	103	2	US-08-920-162A-2	Sequence 2, Appl
743	5	1.5	86	4	US-08-858-207A-470	Sequence 470, App	816	5	1.5	103	3	US-08-783-974-5	Sequence 5, Appl
744	5	1.5	87	2	US-08-446-345-24	Sequence 24, App	817	5	1.5	103	3	US-08-339-708A-10	Sequence 10, Appl
745	5	1.5	87	2	US-08-553-501A-89	Sequence 89, App	818	5	1.5	103	3	US-08-339-708A-12	Sequence 12, Appl
746	5	1.5	87	3	US-09-205-231-89	Sequence 89, App	819	5	1.5	103	3	US-08-747-221B-8	Sequence 8, Appl
747	5	1.5	87	4	US-09-450-072-74	Sequence 74, App	820	5	1.5	103	4	US-09-356-931-2	Sequence 2, Appl
748	5	1.5	88	2	US-08-528-057-6	Sequence 6, Appl	821	5	1.5	103	4	US-09-005-051-8	Sequence 8, Appl
749	5	1.5	89	2	US-08-446-345-28	Sequence 28, App	822	5	1.5	103	4	US-08-703-675C-2	Sequence 2, Appl
750	5	1.5	89	3	US-08-816-977-8	Sequence 8, Appl	823	5	1.5	103	4	US-08-617-267C-2	Sequence 2, Appl
751	5	1.5	91	1	US-08-168-091A-28	Sequence 28, App	824	5	1.5	104	1	US-08-716-58B-1	Sequence 1, Appl
752	5	1.5	92	1	US-08-118-270-341	Sequence 341, App	825	5	1.5	104	2	US-08-801-977-5	Sequence 5, Appl
753	5	1.5	92	5	PCT-US93-08528-341	Sequence 341, App	826	5	1.5	104	2	US-08-966-444-1	Sequence 1, Appl
754	5	1.5	95	1	US-07-847-743B-14	Sequence 14, App	827	5	1.5	104	3	US-09-178-881-5	Sequence 5, Appl
755	5	1.5	95	1	US-08-456-201-14	Sequence 14, App	828	5	1.5	104	3	US-08-654-618-21	Sequence 21, Appl
756	5	1.5	95	1	US-08-438-753B-24	Sequence 24, App	829	5	1.5	104	3	US-08-654-575-7	Sequence 7, Appl
757	5	1.5	95	1	US-08-443-883A-24	Sequence 24, App	830	5	1.5	105	2	US-08-729-345-1	Sequence 1, Appl

831	5	1.5	105	4	US-09-199-637A-337	Sequence 337, App	904	5	1.5	123	2	US-08-290-592E-30	Sequence 30, Appl
832	5	1.5	106	2	US-08-715-554-3	Sequence 3, Appl1	905	5	1.5	123	4	US-09-135-020-111	Sequence 111, App
833	5	1.5	106	2	US-08-583-118-3	Sequence 3, Appl1	906	5	1.5	123	4	US-09-135-010A-111	Sequence 111, App
834	5	1.5	106	2	US-08-341-843B-24	Sequence 29, Appl	907	5	1.5	123	5	PCT-US95-10053-27	Sequence 27, Appl
835	5	1.5	106	2	US-08-427-497E-29	Sequence 24, Appl	908	5	1.5	123	5	PCT-US96-09448-30	Sequence 30, Appl
836	5	1.5	108	1	US-07-743-518-24	Sequence 24, Appl	909	5	1.5	124	1	US-08-462-948-28	Sequence 28, Appl
837	5	1.5	108	2	US-08-330-272-4	Sequence 4, Appl1	910	5	1.5	124	1	US-08-023-764B-28	Sequence 28, Appl
838	5	1.5	108	2	PCT-US95-13663-4	Sequence 4, Appl1	911	5	1.5	124	3	US-08-904-871-10	Sequence 10, Appl
839	5	1.5	108	6	5187153-14	Patent No. 5187153	912	5	1.5	125	1	US-08-473-981A-10	Sequence 10, Appl
840	5	1.5	108	6	5230013-18	Patent No. 5230013	913	5	1.5	125	2	US-08-164-292B-8	Sequence 8, Appl1
841	5	1.5	108	6	5233482-16	Patent No. 5233482	914	5	1.5	125	2	US-08-474-087-10	Sequence 10, Appl
842	5	1.5	109	4	US-09-199-637A-25	Sequence 25, Appl	915	5	1.5	125	3	US-08-845-623-8	Sequence 8, Appl1
843	5	1.5	110	4	US-09-437-054A-6	Sequence 6, Appl1	916	5	1.5	125	3	US-08-815-927-8	Sequence 8, Appl1
844	5	1.5	111	3	US-08-545-809A-98	Sequence 98, Appl	917	5	1.5	125	4	US-09-103-330-8	Sequence 8, Appl1
845	5	1.5	111	3	US-09-091-725-39	Sequence 39, Appl	918	5	1.5	125	4	US-09-314-268-2	Sequence 2, Appl1
846	5	1.5	112	3	US-08-446-919A-5	Sequence 5, Appl1	919	5	1.5	125	4	US-09-199-637A-207	Sequence 207, App
847	5	1.5	112	3	US-08-648-322-2	Sequence 2, Appl1	920	5	1.5	126	1	US-08-202-389-10	Sequence 10, Appl
848	5	1.5	112	4	US-08-737-226-4	Sequence 4, Appl1	921	5	1.5	126	3	US-09-053-197A-11	Sequence 11, Appl
849	5	1.5	112	4	US-09-001-472-3	Sequence 4, Appl1	922	5	1.5	126	3	US-08-718-905-4	Sequence 4, Appl1
850	5	1.5	113	1	US-08-168-091A-26	Sequence 26, Appl	923	5	1.5	126	3	US-09-550-497-4	Sequence 4, Appl1
851	5	1.5	113	2	US-08-630-822A-88	Sequence 88, Appl	924	5	1.5	126	4	US-09-147-992-4	Sequence 4, Appl1
852	5	1.5	113	2	US-09-005-069-88	Sequence 88, Appl	925	5	1.5	126	4	US-09-085-761A-11	Sequence 11, Appl
853	5	1.5	113	2	US-08-997-080-140	Sequence 140, App	926	5	1.5	127	2	US-08-637-759B-334	Sequence 334, App
854	5	1.5	113	2	US-08-997-362-140	Sequence 140, App	927	5	1.5	127	3	US-08-871-355A-334	Sequence 334, App
855	5	1.5	113	4	US-09-095-855-140	Sequence 140, App	928	5	1.5	127	4	US-09-201-945-334	Sequence 334, App
856	5	1.5	113	4	US-08-905-223-450	Sequence 450, App	929	5	1.5	128	2	US-08-759-581B-21	Sequence 21, Appl
857	5	1.5	113	4	US-09-324-542-140	Sequence 140, App	930	5	1.5	128	2	US-08-428-197-15	Sequence 15, Appl
858	5	1.5	113	4	US-08-936-165A-334	Sequence 334, App	931	5	1.5	128	4	US-09-304-711-21	Sequence 21, Appl
859	5	1.5	113	4	US-09-056-556-230	Sequence 230, App	932	5	1.5	128	5	PCT-US93-10555-15	Sequence 15, Appl
860	5	1.5	114	4	US-08-929-856-66	Sequence 66, Appl	933	5	1.5	129	6	5428135-6	Patent No. 5428135
861	5	1.5	114	4	US-08-929-856-189	Sequence 189, App	934	5	1.5	130	6	US-08-253-155A-26	Sequence 26, App
862	5	1.5	114	4	US-09-347-819-4	Sequence 4, Appl1	935	5	1.5	130	2	US-08-726-306A-18	Sequence 18, Appl
863	5	1.5	114	4	US-09-437-054A-2	Sequence 2, Appl1	936	5	1.5	130	3	US-08-894-017-6	Sequence 6, Appl1
864	5	1.5	115	1	US-08-185-414E-3	Sequence 3, Appl1	937	5	1.5	130	3	US-08-838-682-4	Sequence 4, Appl1
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866	5	1.5	115	4	US-08-895-914-8	Sequence 8, Appl1	939	5	1.5	130	4	US-09-357-710A-4	Sequence 4, Appl1
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869	5	1.5	117	3	US-08-965-903B-16	Sequence 16, Appl	942	5	1.5	131	4	US-08-939-093A-2	Sequence 2, Appl1
870	5	1.5	117	4	US-09-228-986-111	Sequence 111, App	943	5	1.5	133	1	US-08-268-348A-8	Sequence 8, Appl1
871	5	1.5	118	3	US-08-301-162-10	Sequence 10, Appl	944	5	1.5	133	1	US-08-268-348A-10	Sequence 10, Appl
872	5	1.5	118	4	US-09-461-240-10	Sequence 10, Appl	945	5	1.5	136	4	US-09-456-830-27	Sequence 27, Appl
873	5	1.5	118	4	US-09-056-556-231	Sequence 231, App	946	5	1.5	136	5	PCT-US95-07117-2	Sequence 2, Appl1
874	5	1.5	119	1	US-08-236-077-4	Sequence 4, Appl1	947	5	1.5	137	3	US-08-851-843A-210	Sequence 210, App
875	5	1.5	119	1	US-08-466-127-4	Sequence 4, Appl1	948	5	1.5	137	4	US-08-974-549A-329	Sequence 329, App
876	5	1.5	119	1	US-08-467-420A-19	Sequence 19, Appl	949	5	1.5	137	4	US-08-854-050-210	Sequence 210, App
877	5	1.5	119	1	US-08-470-110A-19	Sequence 19, Appl	950	5	1.5	137	4	US-09-456-830-45	Sequence 45, Appl
878	5	1.5	119	1	US-08-667-769A-19	Sequence 19, Appl	951	5	1.5	137	4	US-09-456-830-53	Sequence 53, Appl
879	5	1.5	119	2	US-08-840-371-19	Sequence 19, Appl	952	5	1.5	137	4	US-09-456-830-57	Sequence 57, Appl
880	5	1.5	119	3	US-09-045-764A-3	Sequence 3, Appl1	953	5	1.5	137	4	US-09-430-323-210	Sequence 210, App
881	5	1.5	119	3	US-08-637-647-19	Sequence 19, Appl	954	5	1.5	139	1	US-08-278-729A-8	Sequence 8, Appl1
882	5	1.5	119	5	PCT-US95-17082A-19	Sequence 19, Appl	955	5	1.5	139	1	US-08-155-343A-8	Sequence 8, Appl1
883	5	1.5	120	1	US-08-347-492B-2	Sequence 2, Appl1	956	5	1.5	139	1	US-08-406-672-8	Sequence 8, Appl1
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889	5	1.5	120	3	US-09-205-231-90	Sequence 90, Appl	962	5	1.5	139	2	US-08-553-501A-59	Sequence 59, Appl
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891	5	1.5	120	4	US-09-025-769B-23	Sequence 23, Appl	964	5	1.5	139	2	US-08-461-397A-8	Sequence 8, Appl1
892	5	1.5	120	5	PCT-US95-10053-28	Sequence 28, Appl	965	5	1.5	139	2	US-08-912-088-8	Sequence 8, Appl1
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894	5	1.5	120	5	PCT-US96-09448-31	Sequence 31, Appl	967	5	1.5	139	3	US-08-445-467-8	Sequence 8, Appl1
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898	5	1.5	122	2	US-08-820-170A-1	Sequence 1, Appl1	971	5	1.5	139	4	US-08-414-033A-8	Sequence 8, Appl1
899	5	1.5	122	3	US-09-055-699-1	Sequence 1, Appl1	972	5	1.5	139	4	US-08-271-556A-6	Sequence 6, Appl1
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902	5	1.5	123	4	US-08-078-683A-9	Sequence 9, Appl1	975	5	1.5	139	4	US-09-170-936-8	Sequence 8, Appl1
903	5	1.5	123	1	US-08-061-314A-2	Sequence 2, Appl1	976	5	1.5	139	4	US-08-858-207A-429	Sequence 429, App

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997 5 1.5 142 4 US-08-705-347A-47 Sequence 47, Appl1
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999 5 1.5 142 4 US-09-324-542-47 Sequence 47, Appl1
1000 5 1.5 143 2 US-08-834-655-11 Sequence 11, Appl1

ALIGNMENTS

RESULT 1
US-08-651-818A-2
Sequence 2, Application US/08651818A
Patent No. 5948889
GENERAL INFORMATION:
APPLICANT: de Boer, Piet A.J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING
TITLE OF INVENTION: ANTIMICROBIALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,818A
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: CASE-02249
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-08-651-818A-2

Query Match 100.0%; Score 328; DB 2; Length 328;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MMDRLILIIIVGAIATALLVHGFWTSRKERSMFDRPLKRSKRDDSDYDEVEDD 60
QY 61 EGVEVHRVHNVHAPANAQHEAARPSQHOYOPPVASAPROPVQOPPEAOVPPQHAPH 120
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QY 301 LDDQRRMTPOKLRXYODIIRVYKDANA 328
Db 301 LDDQRRMTPOKLRXYODIIRVYKDANA 328

RESULT 2
US-09-184-826-2
Sequence 2, Application US/09184826
Patent No. 6248543
GENERAL INFORMATION:
APPLICANT: de Boer, Piet A.J.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR SCREENING
TITLE OF INVENTION: ANTIMICROBIALS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,826
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: CASE-02249
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 328 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
US-09-184-826-2

Query Match 100.0%; Score 328; DB 4; Length 328;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMDLRLIILIVGAIIIALVHGFWSRKRSSMFRDRPLKMKSRDDSDYDEVEDD 60
Db 1 MMDLRLIILIVGAIIIALVHGFWSRKRSSMFRDRPLKMKSRDDSDYDEVEDD 60
QY 61 EGVGEVVRHVRNHPANAOEHEAARSPQHQPYPYASAPROPVQOPEPAVPH 120
Db 61 EGVGEVVRHVRNHPANAOEHEAARSPQHQPYPYASAPROPVQOPEPAVPH 120
QY 121 PAQVQOAPVQOPEQPLQOVPSPQVAPAPQVHSAPOPQOAFQPAEPVAAPOPEV 180
Db 121 PAQVQOAPVQOPEQPLQOVPSPQVAPAPQVHSAPOPQOAFQPAEPVAAPOPEV 180
QY 181 PAVPMKPKRKEAVIIMNVAHHGSEINGEALLNSIQAGFIFGDMNIYHRLHSPDSC 240
Db 181 PAVPMKPKRKEAVIIMNVAHHGSEINGEALLNSIQAGFIFGDMNIYHRLHSPDSC 240
QY 241 ALFSLANMKPGTFDEPMKDTTPGVYTFMQVPSYSGDELONFKMLQSAQHIAD 300
Db 241 ALFSLANMKPGTFDEPMKDTTPGVYTFMQVPSYSGDELONFKMLQSAQHIAD 300
QY 301 LDDQRRMMPQKLRKYODIIRVYKDANA 328
Db 301 LDDQRRMMPQKLRKYODIIRVYKDANA 328

RESULT 3

US-09-075-272-3
Sequence 3, Application US/09075272
Patent No. 6136598
GENERAL INFORMATION:
APPLICANT: MILLER, A. DUSTY
APPLICANT: WOLGAMOT, GREG
APPLICANT: BONHAM, LYNN
TITLE OF INVENTION: MUS DUNNI ENDOGENOUS RETROVIRAL
TITLE OF INVENTION: PACKAGING CELL LINES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,272
FILING DATE: 08-MAY-1998
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/046,140
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: POOR, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 14538A-003710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 522 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-075-272-3

Query Match 2.7%; Score 9; DB 4; Length 522;

Best Local Similarity 100.0%; Pred. No. 1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 PVAAPOPEP 177
Db 156 PVAAPOPEP 164

RESULT 4

US-09-075-272-2
Sequence 2, Application US/09075272
Patent No. 6136598
GENERAL INFORMATION:
APPLICANT: MILLER, A. DUSTY
APPLICANT: WOLGAMOT, GREG
APPLICANT: BONHAM, LYNN
TITLE OF INVENTION: MUS DUNNI ENDOGENOUS RETROVIRAL
TITLE OF INVENTION: PACKAGING CELL LINES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,272
FILING DATE: 08-MAY-1998
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/046,140
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: POOR, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 14538A-003710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-075-272-2

Query Match 2.7%; Score 9; DB 4; Length 622;

Best Local Similarity 100.0%; Pred. No. 1.2;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 PVAAPOPEP 177
Db 256 PVAAPOPEP 264

RESULT 5

US-09-172-045-2
Sequence 2, Application US/09172045
Patent No. 6277594
GENERAL INFORMATION:
APPLICANT: MIKOSHIBA, Katsuhiko
APPLICANT: Aruga, Jun
APPLICANT: Nagai, Takeharu
APPLICANT: Nakata, Katsunori

FILE REFERENCE: HIRAKI-03497
CURRENT APPLICATION NUMBER: US/09/172.045
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: JP98/86979
EARLIER FILING DATE: 1998-03-31
EARLIER APPLICATION NUMBER: JP98/121456
EARLIER FILING DATE: 1998-04-30
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 441
TYPE: PRT
ORGANISM: Xenopus laevis
US-09-172-045-2

Query Match 2.4%; Score 8; DB 2; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 197 MNVAHHG 204
Db 199 MNVAHHG 206

RESULT 6
US-08-374-483-4
Sequence 4, Application US/08374483
Patent No. 5880102
GENERAL INFORMATION:
APPLICANT: GEORGE, SAMUEL E.
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1015 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-374-483-4

Query Match 2.4%; Score 8; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 176 EPVAEPAP 183
Db 953 EPVAEPAP 960

RESULT 7
US-08-374-483-7
Sequence 7, Application US/08374483
Patent No. 5880102
GENERAL INFORMATION:
APPLICANT: GEORGE, SAMUEL E.
ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-83
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1015 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-374-483-7

Query Match 2.4%; Score 8; DB 2; Length 1015;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 176 EPVAEPAP 183
Db 953 EPVAEPAP 960

RESULT 8
US-08-818-112-142
Sequence 142, Application US/08818112
Patent No. 6290969
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,112
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-818-112-142

Query Match 2.1%; Score 7; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 VAPAPOP 152
DB 244 VAPAPOP 250

RESULT 9
US-08-818-111-137
Sequence 137, Application US/08818111
Patent No. 6338852
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghlon, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
TUBERCULOSIS
NUMBER OF SEQUENCES: 148
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/818,111
FILING DATE: 13-MAR-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.

REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 137:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-818-111-137

Query Match 2.1%; Score 7; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 VAPAPOP 152
DB 244 VAPAPOP 250

RESULT 10
US-09-056-556-142
Sequence 142, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 142:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-056-556-142

Query Match 2.1%; Score 7; DB 4; Length 267;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 146 VAPAPOP 152
DB 244 VAPAPOP 250

Db 244 VAPAPOP 250

RESULT 11
US-08-892-880-3
; Sequence 3, Application US/08892880
; Patent No. 5942417
; GENERAL INFORMATION:
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER L.
; APPLICANT: DILLON, PATRICK J.
; TITLE OF INVENTION: CD44-LIKE PROTEIN
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/892,880
; FILING DATE: HERWITH
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/021,762
; FILING DATE: 15-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.0490001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ. ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-892-880-3

Query Match 2.1%; Score 7; DB 2; Length 339;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 205 SELNGEA 211
|||||||
Db 296 SELNGEA 302

RESULT 12
US-07-946-497-7
; Sequence 7, Application US/07946497
; Patent No. 5506119
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHER, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,497
; FILING DATE: 19921109
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 16915/145
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ. ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 363 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: mCD44
; US-07-946-497-7

Query Match 2.1%; Score 7; DB 1; Length 363;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 205 SELNGEA 211
|||||||
Db 318 SELNGEA 324

RESULT 13
US-08-483-322-7
; Sequence 7, Application US/08483322
; Patent No. 5760178
; GENERAL INFORMATION:
; APPLICANT: HERRLICH, Peter
; APPLICANT: PONTA, Helmut
; APPLICANT: GUENTHER, Ursula
; APPLICANT: MATZKU, Siegfried
; APPLICANT: WENZL, Achim
; TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
; TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,322
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/946,497
; FILING DATE: 09-NOV-1992

ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16915/145
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: mCD44
US-08-483-322-7

Query Match 2.1%; Score 7; DB 1; Length 363;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 SELNGEA 211
|||||
DB 318 SELNGEA 324

RESULT 14
US-08-478-882-7
Sequence 7, Application US/08478882
Patent No. 585575
GENERAL INFORMATION:
APPLICANT: HERRLICH, Peter
APPLICANT: PONTA, Helmut
APPLICANT: GUENTHER, Ursula
APPLICANT: MATZKU, Siegfried
APPLICANT: WENZL, Achim
TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
NUMBER OF INVENTIONS: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,882
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946,497
FILING DATE: 19921109
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16915/145
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 363 amino acids
TYPE: amino acid
TOPOLOGY: linear
IMMEDIATE SOURCE:

CLONE: mCD44
US-08-478-882-7

Query Match 2.1%; Score 7; DB 2; Length 363;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 SELNGEA 211
|||||
DB 318 SELNGEA 324

RESULT 15
US-07-946-497-2
Sequence 2, Application US/07946497
Patent No. 550619
GENERAL INFORMATION:
APPLICANT: HERRLICH, Peter
APPLICANT: PONTA, Helmut
APPLICANT: GUENTHER, Ursula
APPLICANT: MATZKU, Siegfried
APPLICANT: WENZL, Achim
TITLE OF INVENTION: VARIANT CD44 SURFACE PROTEINS, DNA
TITLE OF INVENTION: SEQUENCES CODING THESE, ANTIBODIES AGAINST THESE PROTEINS,
NUMBER OF INVENTIONS: AS WELL AS THEIR USE IN DIAGNOSIS AND THERAPY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,497
FILING DATE: 19921109
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16915/145
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-946-497-2

Query Match 2.1%; Score 7; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 205 SELNGEA 211
|||||
DB 458 SELNGEA 464

Search completed: September 25, 2002, 09:52:55
Job time: 169 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 25, 2002, 09:50:51 : Search time 17.78 Seconds
(without alignments)
1772.627 Million cell updates/sec

Title: US-09-184-826-2

Perfect score: 328
Sequence: 1 MMDLRLILIVGAIALAL.....TPQKLRXYODIRKVDANA 328

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : PIR_71:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	69.2	328	2 C65015	hypothetical prote
2	119	36.3	332	2 D91039	cell division prot
3	117	35.7	328	2 G85883	cell division prot
4	54	16.5	328	2 AB0810	cell division prot
5	11	3.4	328	2 AC0363	probable cell divi
6	9	2.7	137	2 T23308	hypothetical prote
7	8	2.4	130	2 D84353	hypothetical prote
8	8	2.4	339	2 S37920	MBR1 protein precu
9	8	2.4	405	2 AE0990	probable membrane
10	8	2.4	419	1 S47692	hypothetical 43.8K
11	8	2.4	419	2 B91169	probable transport
12	8	2.4	419	2 B86015	probable transport
13	8	2.4	512	2 G86773	hypothetical prote
14	8	2.4	912	2 B97566	citrate (Pro-35)-I
15	8	2.4	1008	2 AH2786	hypothetical prote
16	8	2.4	2485	1 H71621	conserved hypothet
17	7	2.1	49	2 S23290	serine/threonine-s
18	7	2.1	82	2 G84456	light-harvesting p
19	7	2.1	176	2 T26212	hypothetical prote
20	7	2.1	186	2 T31951	hypothetical prote
21	7	2.1	202	2 T15874	hypothetical prote
22	7	2.1	206	2 A84236	30S ribosomal prot
23	7	2.1	212	2 E81669	conserved hypothet
24	7	2.1	213	2 E71511	hypothetical prote
25	7	2.1	246	2 A70124	hypothetical prote
26	7	2.1	250	2 T14000	aquaporin T1P7 - c
27	7	2.1	253	2 AC0654	hypothetical oxido
28	7	2.1	271	2 D71103	probable homoserin
29	7	2.1	272	2 E83363	hypothetical prote

30	7	2.1	278	1 TPRH7W	tiropontin T, slow s
31	7	2.1	285	2 C98105	hypothetical prote
32	7	2.1	285	2 B95241	conserved hypothet
33	7	2.1	288	2 E64202	fructose-bisphosph
34	7	2.1	289	2 E83454	cell division prot
35	7	2.1	290	2 B83924	hypothetical prote
36	7	2.1	291	2 T48880	beta-lactamase (EC
37	7	2.1	290	2 E82258	cell division prot
38	7	2.1	304	2 T42521	probable UTP--gluc
39	7	2.1	312	2 C82208	siroheme synthase
40	7	2.1	328	2 D84030	delta-aminolevulin
41	7	2.1	340	2 A72600	probable dehydroge
42	7	2.1	356	2 JQ2352	glycoprotein I - t
43	7	2.1	356	2 G82523	endo-1,4-beta-gluc
44	7	2.1	358	2 G81822	translation releas
45	7	2.1	358	2 G81053	translation releas
46	7	2.1	362	2 A35616	T-cell surface gly
47	7	2.1	363	2 A37009	CD44 homolog membr
48	7	2.1	365	2 A34424	CD44 membrane gly
49	7	2.1	372	2 T38192	hypothetical prote
50	7	2.1	380	2 G86656	ABC transporter pe
51	7	2.1	396	2 B75186	hypothetical prote
52	7	2.1	404	2 B89819	hypothetical prote
53	7	2.1	455	2 A87913	pyrimidine nucleo
54	7	2.1	460	2 S01508	protein B9205.10 l
55	7	2.1	461	2 T11800	NADH dehydrogenase
56	7	2.1	482	2 A39132	NADH dehydrogenase
57	7	2.1	485	2 T19394	anthranilate synth
58	7	2.1	487	1 OOEGRS	hypothetical prote
59	7	2.1	502	2 H75290	YggE protein - Bac
60	7	2.1	502	2 A70988	hypothetical prote
61	7	2.1	503	2 B38745	hypothetical prote
62	7	2.1	505	2 T40935	cell adhesion mole
63	7	2.1	525	2 JN0443	probable utp--gluc
64	7	2.1	548	2 E70546	transcription init
65	7	2.1	562	2 T15131	hypothetical prote
66	7	2.1	583	2 C97610	hypothetical prote
67	7	2.1	583	2 AG2832	cell division prot
68	7	2.1	609	2 G87496	peptidase, M23/M37
69	7	2.1	615	2 T29550	hypothetical prote
70	7	2.1	693	2 C87575	sensor histidine k
71	7	2.1	736	2 A86171	hypothetical prote
72	7	2.1	745	2 G72453	hypothetical prote
73	7	2.1	762	2 H87302	chemotaxis protein
74	7	2.1	802	2 S42518	PML protein, spli
75	7	2.1	802	2 S44382	PML protein, spli
76	7	2.1	874	2 T34922	phosphoenolpyruvat
77	7	2.1	880	2 D89756	protein T337.2b l
78	7	2.1	899	2 C95339	hypothetical prote
79	7	2.1	1006	2 JC5526	hypothetical prote
80	7	2.1	1018	1 S73720	kinase-defective E
81	7	2.1	1073	2 S56220	cytadherence acces
82	7	2.1	1242	2 T20739	probable membrane
83	7	2.1	1420	2 T37281	hypothetical prote
84	7	2.1	1448	2 F83237	probable cytoskele
85	7	2.1	1782	2 S45289	probable ATP-depen
86	7	2.1	2777	2 D96746	vitellogenin precu
87	7	2.1	6359	2 T31679	hypothetical prote
88	7	2.1	16	2 PH0754	bacteraicin synthet
89	6	1.8	16	2 C93174	T-cell receptor be
90	6	1.8	39	2 T12912	avenacin - oat (fr
91	6	1.8	41	2 T07236	hypothetical prote
92	6	1.8	41	2 H64039	photosystem I psbJ
93	6	1.8	44	2 B38075	hypothetical prote
94	6	1.8	47	2 AE3429	N-acetylglactosam
95	6	1.8	53	2 F90763	hypothetical prote
96	6	1.8	53	2 D82553	hypothetical prote
97	6	1.8	57	2 PN0624	alpha-internexin -
98	6	1.8	57	2 E82733	hypothetical prote
99	6	1.8	70	2 A83982	hypothetical prote
100	6	1.8	71	2 S45608	light-harvesting p
101	6	1.8	73	2 G95106	hypothetical prote
102	6	1.8	75	2 AG1731	hypothetical prote

103	6	1.8	79	2	AC0509	oxaloacetate decar	176	6	1.8	146	2	A10450	conserved hypoteth
104	6	1.8	80	2	AF0909	oxaloacetate decar	177	6	1.8	147	2	A70462	ribosomal protein
105	6	1.8	82	2	EB7465	host factor-I prot	178	6	1.8	147	2	F72730	yhcv homolog APE03
106	6	1.8	90	2	A38934	porphobilinogen sy	179	6	1.8	148	2	T03982	5-epi-aristoloch
107	6	1.8	90	2	G75509	hypothetical prote	180	6	1.8	148	2	T31040	conserved hypoteth
108	6	1.8	91	2	T17968	hypothetical prote	181	6	1.8	148	2	H75096	hypothetical prote
109	6	1.8	92	2	D72223	conserved hypoteth	182	6	1.8	149	2	E90655	hypothetical prote
110	6	1.8	92	2	S21307	hypothetical prote	183	6	1.8	151	2	F82427	hypothetical prote
111	6	1.8	93	2	E72581	hypothetical prote	184	6	1.8	151	2	T10768	latex allergen Hsv
112	6	1.8	92	2	S72254	ribosomal protein	185	6	1.8	151	2	F85506	hypothetical prote
113	6	1.8	94	2	B82847	hypothetical prote	186	6	1.8	156	2	E64084	hypothetical prote
114	6	1.8	95	1	FEIV	ferredoxin [2Fe-2S	187	6	1.8	156	2	T20267	kdib protein - Hae
115	6	1.8	97	2	F70939	hypothetical prote	188	6	1.8	156	2	T30413	hypothetical prote
116	6	1.8	98	2	S69086	cystatin A - bovin	189	6	1.8	157	2	C71814	lipopolysaccharide
117	6	1.8	98	2	T44883	hypothetical prote	190	6	1.8	157	2	C64704	lipopolysaccharide
118	6	1.8	100	2	S53467	hypothetical prote	191	6	1.8	158	2	G81347	3-deoxy-D-manno-oc
119	6	1.8	100	2	T36231	probable dehydroge	192	6	1.8	159	2	JU0468	kdib protein - Eac
120	6	1.8	100	2	G81749	hypothetical prote	193	6	1.8	159	2	E91192	phosphopantetheine
121	6	1.8	100	2	C72690	hypothetical prote	194	6	1.8	159	2	A83600	phosphopantetheine
122	6	1.8	100	2	E91280	cytochrome b(562)	195	6	1.8	159	2	F86039	probable enzyme of
123	6	1.8	100	2	E86121	cytochrome b (562)	196	6	1.8	159	2	AF0007	pantetheine-phosph
124	6	1.8	100	2	AG0279	acetylactate synth	197	6	1.8	159	2	AH0971	pantetheine-phosph
125	6	1.8	101	2	A36869	probable export pr	198	6	1.8	159	2	T51520	hypothetical prote
126	6	1.8	101	2	F90964	flagellar protein	199	6	1.8	160	1	S14574	globin C precursor
127	6	1.8	101	2	F85812	flagellar biosynthe	200	6	1.8	160	2	AD1331	phosphopantetheine
128	6	1.8	103	2	AF0031	probable membrane	201	6	1.8	160	2	S65978	spore coat protein
129	6	1.8	103	2	AB2694	hypothetical prote	202	6	1.8	160	2	E95882	hypothetical trans
130	6	1.8	104	2	A60094	neurofilament-M ho	203	6	1.8	160	2	G90168	conserved hypoteth
131	6	1.8	107	2	T44532	hypothetical prote	204	6	1.8	161	1	JT0292	hemoglobin VIB-5/
132	6	1.8	108	2	G84522	similar to gibbere	205	6	1.8	161	1	JT0349	hemoglobin VIB-5
133	6	1.8	110	2	B69403	hypothetical prote	206	6	1.8	161	1	A30477	hemoglobin VIB-6
134	6	1.8	110	2	G72597	hypothetical prote	207	6	1.8	161	1	S04499	hemoglobin VIB-8
135	6	1.8	111	2	A71507	probable L22 ribos	208	6	1.8	161	1	S04500	hemoglobin VIB-9
136	6	1.8	112	2	G72645	hypothetical prote	209	6	1.8	161	1	S14576	globin E precursor
137	6	1.8	112	2	H95198	hypothetical prote	210	6	1.8	161	2	A95049	acetyl-CoA carboxy
138	6	1.8	117	2	C69969	hypothetical prote	211	6	1.8	161	2	G97919	lipopolysaccharide
139	6	1.8	118	2	F98065	hypothetical prote	212	6	1.8	161	2	B70323	lipopolysaccharide
140	6	1.8	118	2	F75445	hypothetical prote	213	6	1.8	161	2	AD1702	lipopolysaccharide
141	6	1.8	122	2	G65840	conserved hypoteth	214	6	1.8	161	2	AF0013	S-adenosylmethionl
142	6	1.8	124	2	A47582	B-cell growth fact	215	6	1.8	162	2	C82738	lipopolysaccharide
143	6	1.8	126	2	I61260	synapsin II - mous	216	6	1.8	162	2	D98020	conserved hypoteth
144	6	1.8	127	2	AI0329	conserved hypoteth	217	6	1.8	162	2	H70927	probable rpsp prot
145	6	1.8	127	2	F81026	hypothetical prote	218	6	1.8	163	1	S21632	hemoglobin Z precu
146	6	1.8	127	2	F95968	hypothetical prote	219	6	1.8	163	2	D87445	hypothetical prote
147	6	1.8	128	1	CBEC62	cytochrome b562 pr	220	6	1.8	163	2	T25347	hypothetical prote
148	6	1.8	128	1	AF0449	probable cytochrom	221	6	1.8	163	2	AD0462	probable exported
149	6	1.8	128	2	AF1056	soluble cytochrome	222	6	1.8	164	2	H82347	lipopolysaccharide
150	6	1.8	128	2	T32947	hypothetical prote	223	6	1.8	164	2	A12183	hypothetical prote
151	6	1.8	129	2	AH1458	B. subtilis YabA p	224	6	1.8	165	2	S44302	single-stranded DN
152	6	1.8	130	2	AE2472	hypothetical prote	225	6	1.8	165	2	H84997	hypothetical prote
153	6	1.8	131	2	AH0348	probable membrane	226	6	1.8	166	2	AD1744	low temperature re
154	6	1.8	132	2	T18095	trans-regulatory s	227	6	1.8	166	2	AF1374	B. subtilis YutG p
155	6	1.8	133	1	F45345	hypothetical prote	228	6	1.8	167	2	D82561	probable signal pe
156	6	1.8	134	2	E81133	hypothetical prote	229	6	1.8	168	2	AF2620	conserved hypoteth
157	6	1.8	135	2	E70585	probable transcrip	230	6	1.8	168	2	AG2257	hypothetical prote
158	6	1.8	136	2	B96504	protein F9C16.21 l	231	6	1.8	169	2	I55299	cytochrome P450 PB
159	6	1.8	136	2	H83312	probable type II s	232	6	1.8	169	2	S72166	lipopolysaccharide
160	6	1.8	138	1	DMRC	desmin - pig (frag	233	6	1.8	169	2	H84077	low temperature re
161	6	1.8	138	2	E95917	hypothetical proli	234	6	1.8	170	2	E86341	F9H16.13 protein -
162	6	1.8	139	2	A64412	hypothetical prote	235	6	1.8	172	2	T12202	probable cdc2-like
163	6	1.8	139	2	H81886	hypothetical prote	236	6	1.8	174	2	JC1294	pape fibrillar prot
164	6	1.8	139	2	H81812	hypothetical prote	237	6	1.8	174	2	T21945	hypothetical prote
165	6	1.8	139	2	S42605	conserved hypoteth	238	6	1.8	175	2	JE0350	Anterior gradient-
166	6	1.8	140	2	C70223	conserved hypoteth	239	6	1.8	175	2	D86180	hypothetical prote
167	6	1.8	142	1	WMAD19	early E1B 17K prot	240	6	1.8	176	2	JT0616	adenine phosphorib
168	6	1.8	142	2	AB0940	probable membrane	241	6	1.8	179	2	D64591	hypothetical prote
169	6	1.8	143	2	H71641	hypothetical prote	242	6	1.8	179	2	H71920	adenine phosphorib
170	6	1.8	143	2	H83894	hypothetical prote	243	6	1.8	180	2	F97402	hypothetical prote
171	6	1.8	143	2	B53045	translational initia	244	6	1.8	180	2	C72676	hypothetical prote
172	6	1.8	144	2	G86293	40S ribosomal prot	245	6	1.8	180	2	S06616	hypothetical prote
173	6	1.8	144	2	C98131	hypothetical prote	246	6	1.8	181	2	S23521	oleosin - common s
174	6	1.8	144	2	AF3156	hypothetical prote	247	6	1.8	181	2	E83436	probable oxidase p
175	6	1.8	145	2	C84370	cytochrome c oxida	248	6	1.8	183	2	A10710	probable nitroredu

249	6	1.8	184	2	S78091	322	6	1.8	232	2	D71218	hypothetical prote
250	6	1.8	184	2	A70149	323	6	1.8	232	2	G89025	protein F13A2.8 (1
251	6	1.8	185	2	T25891	324	6	1.8	232	2	T17553	hypothetical prote
252	6	1.8	185	2	I40490	325	6	1.8	232	2	AB1908	hypothetical prote
253	6	1.8	187	2	B86704	326	6	1.8	233	2	AG2538	hypothetical prote
254	6	1.8	189	2	H83281	327	6	1.8	234	2	T00931	hypothetical prote
255	6	1.8	190	2	AG0579	328	6	1.8	234	2	AB3335	probable membrane-
256	6	1.8	190	2	C90260	329	6	1.8	237	1	B42371	regulatory protein
257	6	1.8	191	2	A72536	330	6	1.8	237	2	D95113	O-methyltransferase
258	6	1.8	191	2	AB2225	331	6	1.8	237	2	T30028	hypothetical prote
259	6	1.8	191	2	J01919	332	6	1.8	237	2	C97982	conserved hypotet
260	6	1.8	191	2	AE0412	333	6	1.8	238	2	AB4059	16S pseudouridyat
261	6	1.8	193	2	JC2439	334	6	1.8	238	2	C70321	Rieske iron-sulfur
262	6	1.8	193	2	AD2402	335	6	1.8	239	2	F96908	uncharacterized co
263	6	1.8	194	2	S21859	336	6	1.8	239	2	B72573	hypothetical prote
264	6	1.8	197	2	F83846	337	6	1.8	240	2	H69932	hypothetical prote
265	6	1.8	197	2	C90671	338	6	1.8	240	2	S77884	hypothetical prote
266	6	1.8	197	2	G85521	339	6	1.8	241	2	S75347	hypothetical prote
267	6	1.8	197	2	F70832	340	6	1.8	242	2	I40084	glcK protein - Bac
268	6	1.8	197	2	B81720	341	6	1.8	243	2	I50483	vimentin A2 - gold
269	6	1.8	197	2	T35766	342	6	1.8	243	2	S37772	ankyrin, erythrocy
270	6	1.8	198	2	A96520	343	6	1.8	243	2	B61190	mast cell growth f
271	6	1.8	198	2	AG2530	344	6	1.8	245	2	A72275	hypothetical prote
272	6	1.8	200	1	Q08E27	345	6	1.8	245	2	G87215	probable secreted
273	6	1.8	200	2	E64756	346	6	1.8	247	2	S59523	crucose-phosphate 1
274	6	1.8	200	2	G68307	347	6	1.8	247	2	C83296	hypothetical prote
275	6	1.8	202	2	E87497	348	6	1.8	249	2	S59404	hypothetical prote
276	6	1.8	201	2	AD2503	349	6	1.8	250	2	JC7669	acylglycerol lipas
277	6	1.8	201	2	A13484	350	6	1.8	251	2	S25186	probable dehydroge
278	6	1.8	202	2	T11895	351	6	1.8	252	1	A34702	hypothetical prote
279	6	1.8	203	2	E81449	352	6	1.8	253	1	H65046	amphitregulin precu
280	6	1.8	203	2	T24537	353	6	1.8	253	2	B69758	hypothetical prote
281	6	1.8	204	2	S63655	354	6	1.8	253	2	A49122	conserved hypotet
282	6	1.8	205	1	ASLJIK	355	6	1.8	253	2	JC5347	homobox protein M
283	6	1.8	205	2	C75155	356	6	1.8	253	2	T52380	cd3 protein - Cio
284	6	1.8	208	2	T47735	357	6	1.8	254	1	S39876	zinc finger protei
285	6	1.8	208	2	C83742	358	6	1.8	254	1	S39876	gufa protein - Myx
286	6	1.8	211	2	S28046	359	6	1.8	254	2	A31488	flagellin - mouse
287	6	1.8	213	2	S25647	360	6	1.8	257	2	C72727	probable ribosomal
288	6	1.8	213	2	E83866	361	6	1.8	257	2	S65958	mau protein - Par
289	6	1.8	213	2	JC1152	362	6	1.8	258	1	DHMS	Ig delta chain C r
290	6	1.8	215	2	S78275	363	6	1.8	258	1	F69374	conserved hypotet
291	6	1.8	215	2	D84382	364	6	1.8	258	2	S10323	type II site-spect
292	6	1.8	215	2	D75342	365	6	1.8	258	2	T17895	adenosinetriphosph
293	6	1.8	216	2	B96946	366	6	1.8	260	2	I51544	MHC class II beta-
294	6	1.8	216	2	A37762	367	6	1.8	260	2	I51542	MHC class II beta-
295	6	1.8	217	2	D95162	368	6	1.8	260	2	S71507	restriction endonu
296	6	1.8	217	2	C98028	369	6	1.8	260	2	T48846	creatininase (EC 3
297	6	1.8	217	2	C86839	370	6	1.8	261	2	AF1679	hypothetical prote
298	6	1.8	218	2	T49841	371	6	1.8	261	2	T30170	hypothetical prote
299	6	1.8	219	2	B43772	372	6	1.8	262	2	AE1071	feric iron reduct
300	6	1.8	219	2	E75219	373	6	1.8	262	2	T27381	hypothetical prote
301	6	1.8	219	2	E87673	374	6	1.8	263	2	T39487	hypothetical prote
302	6	1.8	221	2	T45044	375	6	1.8	264	2	T30391	hypothetical prote
303	6	1.8	221	2	A13631	376	6	1.8	264	2	D70912	probable monooxyge
304	6	1.8	222	2	T34060	377	6	1.8	266	2	AB1360	probable disulfide
305	6	1.8	222	2	A49955	378	6	1.8	266	2	S02510	nifW protein - Kle
306	6	1.8	223	2	A87483	379	6	1.8	267	2	JC6326	2-hydroxypenta-2,4
307	6	1.8	224	2	T14841	380	6	1.8	268	2	H83508	probable flagellar
308	6	1.8	224	2	T37156	381	6	1.8	268	2	AB2498	hypothetical prote
309	6	1.8	225	2	C90591	382	6	1.8	269	2	I51539	MHC class II beta-
310	6	1.8	226	2	T30695	383	6	1.8	269	2	I51540	MHC class II beta-
311	6	1.8	227	2	G70555	384	6	1.8	269	2	G72550	probable gufa prot
312	6	1.8	227	2	AC0359	385	6	1.8	270	2	I51543	MHC class II beta-
313	6	1.8	228	2	T16678	386	6	1.8	270	2	AH0715	probable inner mem
314	6	1.8	228	2	H69025	387	6	1.8	270	2	S61620	probable membrane
315	6	1.8	228	2	F87670	388	6	1.8	270	2	F95962	probable taurin up
316	6	1.8	228	2	B84178	389	6	1.8	271	2	H83622	hypothetical prote
317	6	1.8	228	2	A96918	390	6	1.8	272	1	S39680	hydroxyethylthiaz
318	6	1.8	229	2	T27466	391	6	1.8	273	2	S05207	vimentin - pig (fr
319	6	1.8	230	2	T15381	392	6	1.8	273	2	A71142	probable UDP-N-ace
320	6	1.8	230	2	G82579	393	6	1.8	273	2	H81927	hypothetical prote
321	6	1.8	231	2	C83300	394	6	1.8	273	2	H81177	conserved hypotet

395	6	1.8	273	2	A35974	mast cell growth f
396	6	1.8	273	2	A84332	hypothetical prot
397	6	1.8	274	1	A41461	fibronectin-bindin
398	6	1.8	274	2	G83214	probable ATP-bind
399	6	1.8	274	2	AC2299	cobalt transport A
400	6	1.8	275	2	T03113	hypothetical prote
401	6	1.8	275	2	T42747	hypothetical prote
402	6	1.8	276	2	E95948	hypothetical prote
403	6	1.8	278	2	E82965	hypothetical prote
404	6	1.8	281	2	D71545	probable oligopept
405	6	1.8	283	2	AF2569	hypothetical prote
406	6	1.8	284	2	E89697	protein F48F7.2 [i
407	6	1.8	284	2	B84118	stage II sporulat
408	6	1.8	285	2	T29832	hypothetical prote
409	6	1.8	286	2	E86844	shikimate 5-dehydr
410	6	1.8	286	2	G86950	probable ABC-trans
411	6	1.8	287	2	G81699	peptide ABC transp
412	6	1.8	288	2	S69661	hypothetical prote
413	6	1.8	288	2	F64448	methyloxygen-red
414	6	1.8	288	2	A13400	serine hydroxymeth
415	6	1.8	290	1	WMBEAK	38K phosphoprotein
416	6	1.8	290	1	WMBEIM	38K phosphoprotein
417	6	1.8	290	2	JN0576	carbonate dehydrat
418	6	1.8	290	2	S45349	L1 metallo-beta-la
419	6	1.8	291	1	DHMSM	Ig delta chain C r
420	6	1.8	291	2	AF1722	post-translocation
421	6	1.8	292	2	D64118	cytidine deaminase
422	6	1.8	292	2	F81430	homoserine kinase
423	6	1.8	293	2	S77419	hypothetical prote
424	6	1.8	293	2	T39396	hypothetical prote
425	6	1.8	293	2	AC1352	post-translocation
426	6	1.8	294	1	KFMS3	tissue factor prec
427	6	1.8	294	2	S51008	protein kinase (EC
428	6	1.8	295	2	AD3577	sugar transport sy
429	6	1.8	295	2	S23585	carboxyphosphoen
430	6	1.8	297	1	S41533	UTP--glucose-1-pho
431	6	1.8	297	1	WM529	homeotic protein H
432	6	1.8	297	2	AC0615	conserved hypotet
433	6	1.8	297	2	JC5699	Down syndrome crit
434	6	1.8	298	1	DMHF	deslun - golden ha
435	6	1.8	298	2	T22390	hypothetical prote
436	6	1.8	298	2	S69241	Dreg-5 protein - f
437	6	1.8	298	2	E90550	conserved hypotet
438	6	1.8	298	2	JC5698	Down syndrome crit
439	6	1.8	299	2	T08460	hypothetical prote
440	6	1.8	299	2	AH0245	probable 4-dihosp
441	6	1.8	299	2	A69229	hypothetical prote
442	6	1.8	299	2	A57652	cyclic nucleotide-
443	6	1.8	299	2	A83841	integrase/recombin
444	6	1.8	300	2	B56118	vetispiradiene syn
445	6	1.8	300	2	AH1357	hypothetical prote
446	6	1.8	300	2	AH1727	hypothetical prote
447	6	1.8	301	2	C72359	conserved hypotet
448	6	1.8	301	2	H75470	histone deacetylase
449	6	1.8	301	2	A70731	probable glyceralp
450	6	1.8	301	2	D83970	UDP-N-acetylenolp
451	6	1.8	302	2	T04109	protein kinase cdc
452	6	1.8	302	2	F81016	conserved hypotet
453	6	1.8	303	2	S12867	carbonate dehydrat
454	6	1.8	303	2	A28620	magnanin precursor
455	6	1.8	303	2	E98226	nicotinate-monomuc
456	6	1.8	303	2	E83131	probable transcrip
457	6	1.8	303	2	C70808	hypothetical prote
458	6	1.8	303	2	T25778	hypothetical prote
459	6	1.8	303	2	A49072	bottleneck - fruit
460	6	1.8	304	2	S02284	potassium channel
461	6	1.8	305	2	F72456	hydroxymethylbilan
462	6	1.8	305	2	T41040	conserved hypotet
463	6	1.8	307	2	D86838	hypothetical prote
464	6	1.8	307	2	G69501	UDP-glucose 4-epim
465	6	1.8	307	2	S75469	menaquinone biosyn
466	6	1.8	307	2	A27389	catechol 2,3-dioxy
467	6	1.8	307	2	A42733	catechol 2,3-dioxy
<hr/>						
468	6	1.8	307	2	J00182	catechol 2,3-dioxy
469	6	1.8	307	2	S47421	catechol 2,3-dioxy
470	6	1.8	307	2	S42100	catechol 2,3-dioxy
471	6	1.8	307	2	T48166	hypothetical prote
472	6	1.8	307	2	G97378	hypothetical prote
473	6	1.8	307	2	AE2596	long protein [impo
474	6	1.8	308	2	JC4137	catechol 2,3-dioxy
475	6	1.8	308	2	H96827	protein F20B17.12
476	6	1.8	309	1	DNECRS	terminator sequenc
477	6	1.8	309	2	D90918	hypothetical prote
478	6	1.8	309	2	A85767	hypothetical prote
479	6	1.8	309	2	AH0690	DNA replication te
480	6	1.8	309	2	AF0451	maltoase operon per
481	6	1.8	309	2	E96566	F6D8.20 [imported]
482	6	1.8	310	2	E90231	UDP-glucose 4-epim
483	6	1.8	310	2	AC0854	probable LysR-famI
484	6	1.8	310	2	D70745	hypothetical prote
485	6	1.8	311	2	AB1880	hypothetical prote
486	6	1.8	312	2	T33344	hypothetical prote
487	6	1.8	312	2	AB2063	hypothetical prote
488	6	1.8	313	2	H97585	carbohydrate kinas
489	6	1.8	313	2	A12806	carbohydrate kinas
490	6	1.8	314	2	S35314	transcription fact
491	6	1.8	315	2	S11081	Na+/K+-exchanging
492	6	1.8	315	2	S76267	hypothetical prote
493	6	1.8	315	2	AD3547	ribose transport s
494	6	1.8	316	2	T09591	probable cdc2-like
495	6	1.8	319	2	H69220	phosphoreactivation-
496	6	1.8	320	1	A39724	homeotic protein H
497	6	1.8	320	2	S41858	hypothetical prote
498	6	1.8	320	2	F75348	hypothetical prote
499	6	1.8	320	2	E71139	hypothetical prote
500	6	1.8	320	2	S18334	lamin C - mouse (f
501	6	1.8	320	2	G86830	thioredoxin reduct
502	6	1.8	321	2	F82104	outer membrane pro
503	6	1.8	321	2	B72604	hypothetical prote
504	6	1.8	321	2	F81030	ABC transporter, p
505	6	1.8	321	2	F81976	probable ferric en
506	6	1.8	322	2	S23053	sloppy paired prot
507	6	1.8	323	1	QXK11M	NADH dehydrogenase
508	6	1.8	324	2	A69648	2-keto-3-deoxygluc
509	6	1.8	325	2	AE1947	hypothetical prote
510	6	1.8	325	2	S37788	PIR3 protein - yea
511	6	1.8	325	2	T41921	hypothetical prote
512	6	1.8	326	2	S67249	probable membrane
513	6	1.8	327	2	I60169	gonadotropin-relae
514	6	1.8	327	2	E64188	dipeptide transpor
515	6	1.8	327	2	D75196	hypothetical prote
516	6	1.8	327	2	S30405	hypothetical prote
517	6	1.8	328	2	A82180	chemotaxis protein
518	6	1.8	328	2	JC4800	P2Y6 receptor - hu
519	6	1.8	328	2	D83197	conserved hydrohet
520	6	1.8	328	2	D81961	probable hypotet
521	6	1.8	328	2	E64020	hypothetical prote
522	6	1.8	329	1	F66905	probable alcohol d
523	6	1.8	329	2	T37891	delta-aminolevulin
524	6	1.8	330	2	B95394	hypothetical prote
525	6	1.8	330	2	AH0938	cell division prot
526	6	1.8	330	2	B97368	hypothetical prote
527	6	1.8	330	2	AB2586	hypothetical sugar
528	6	1.8	331	2	T32322	pfla family carboh
529	6	1.8	331	2	A11879	hypothetical prote
530	6	1.8	333	2	T21595	hypothetical prote
531	6	1.8	333	2	AG3254	glucose-fructose o
532	6	1.8	334	2	S47762	dipeptide transpor
533	6	1.8	334	2	G71228	hypothetical prote
534	6	1.8	334	2	D91181	hypothetical prote
535	6	1.8	334	2	A83662	transcription regu
536	6	1.8	335	2	H86027	hypothetical prote
537	6	1.8	335	2	T31559	hypothetical prote
538	6	1.8	335	2	T31560	hypothetical prote
539	6	1.8	335	2	T31561	hypothetical prote
540	6	1.8	335	2	T41426	hypothetical wtf8

541	6	1.8	335	2	D83142	hypothetical prote
542	6	1.8	335	2	E89819	hypothetical prote
543	6	1.8	336	2	T25180	hypothetical prote
544	6	1.8	336	2	T23902	hypothetical prote
545	6	1.8	336	2	F95925	probable cell-wall
546	6	1.8	337	2	B98333	ribose ABC transp
547	6	1.8	337	2	A12949	hypothetical prote
548	6	1.8	337	2	E82727	glucose kinase Xf1
549	6	1.8	337	2	AC0668	tellurite resistan
550	6	1.8	337	2	A10983	dipeptide transpor
551	6	1.8	338	2	C87311	conserved hypotet
552	6	1.8	339	2	T24007	hypothetical prote
553	6	1.8	339	2	JC7712	transcription coac
554	6	1.8	341	2	A13425	ribose transport s
555	6	1.8	341	2	B82790	conserved hypotet
556	6	1.8	341	2	C89789	hypothetical prote
557	6	1.8	341	2	AG1566	glucitol dehydroge
558	6	1.8	343	2	C84870	probable splicing
559	6	1.8	344	2	A86661	transcription regu
560	6	1.8	344	2	I45774	odorant receptor 1
561	6	1.8	344	2	C97911	hypothetical prote
562	6	1.8	345	2	T24533	hypothetical prote
563	6	1.8	345	2	F98298	pantoate--beta-ala
564	6	1.8	346	2	C83954	MCP-glutamate meth
565	6	1.8	346	2	AH3563	ribose transport s
566	6	1.8	346	2	F75457	conserved hypotet
567	6	1.8	346	2	T44327	hypothetical prote
568	6	1.8	348	2	T37321	Ca2+/calmodulin-de
569	6	1.8	349	2	S67858	gumI protein - Xan
570	6	1.8	352	2	E83519	guinolinate synthet
571	6	1.8	353	2	A95312	probable epoxide h
572	6	1.8	354	2	T36559	hypothetical prote
573	6	1.8	354	2	C83577	acyl-COA dehydroge
574	6	1.8	355	2	B87473	anthranilate phosp
575	6	1.8	355	2	S17704	class I histocompa
576	6	1.8	355	2	B40730	hypothetical prote
577	6	1.8	355	2	S50372	integrinase/recombin
578	6	1.8	356	2	C95134	hypothetical prote
579	6	1.8	356	2	F98002	hypothetical prote
580	6	1.8	357	2	A86825	hypothetical prote
581	6	1.8	357	2	H65041	hypothetical prote
582	6	1.8	357	2	D86707	ABC transporter pe
583	6	1.8	357	2	T24137	hypothetical prote
584	6	1.8	359	2	C97524	hypothetical prote
585	6	1.8	359	2	AD2743	conserved hypotet
586	6	1.8	360	2	C87845	protein T22C1.11 l
587	6	1.8	362	1	LPGCRA	rare lipoprotein A
588	6	1.8	362	2	G90712	a minor lipoprotei
589	6	1.8	362	2	C85563	hypothetical prote
590	6	1.8	363	2	AC3192	hypothetical prote
591	6	1.8	363	2	B75132	cell division cont
592	6	1.8	363	2	C71073	hypothetical prote
593	6	1.8	363	2	T47588	hypothetical prote
594	6	1.8	364	2	AE2184	extracellular solu
595	6	1.8	365	2	B75398	hypothetical prote
596	6	1.8	366	2	D96649	hypothetical prote
597	6	1.8	366	2	T36035	ion transport prot
598	6	1.8	367	2	S49009	fork head protein
599	6	1.8	367	2	T47517	nuclear receptor b
600	6	1.8	369	2	H88535	protein B0523.4 f1
601	6	1.8	370	2	A60089	transforming prote
602	6	1.8	370	2	S49008	fork head protein
603	6	1.8	370	2	A12355	hypothetical prote
604	6	1.8	372	1	C70658	probable pepo - My
605	6	1.8	373	2	G64300	2-hydroxyglutaryl-
606	6	1.8	374	2	B95871	probable CDP-tyrel
607	6	1.8	374	2	D81715	conserved hypotet
608	6	1.8	376	2	A86974	probable cytoplasm
609	6	1.8	377	1	B0A658	virB10 protein - A
610	6	1.8	377	2	A82713	triacylglycerol 11
611	6	1.8	377	2	AF3249	component of type
612	6	1.8	378	2	B27718	cytochrome P450 2C
613	6	1.8	378	2	H70548	hypothetical prote
614	6	1.8	378	2	AH0420	Phm protein [lipo
615	6	1.8	379	2	B55522	lipoprotein D prec
616	6	1.8	379	2	D91078	probable lipoprote
617	6	1.8	379	2	E85923	lipoprotein [lipo
618	6	1.8	380	2	T11803	ubiquinol--cytochr
619	6	1.8	380	2	E84644	hypothetical prote
620	6	1.8	380	2	EA8244	response regulator
621	6	1.8	381	2	T22334	hypothetical prote
622	6	1.8	381	2	E64050	N-acetylglucosamin
623	6	1.8	381	2	T08722	hypothetical prote
624	6	1.8	383	2	H71848	probable nat+/h+ an
625	6	1.8	383	2	G64667	NA+/H+ antiporter
626	6	1.8	384	2	D87471	ROK family protein
627	6	1.8	385	1	S01511	ubiquinol--cytochr
628	6	1.8	385	2	G89956	hypothetical prote
629	6	1.8	385	2	E96797	hypothetical prote
630	6	1.8	386	2	S52981	lycopen cyclase -
631	6	1.8	386	2	C87549	hypothetical prote
632	6	1.8	387	2	E83679	multidrug-efflux t
633	6	1.8	388	2	EA8245	cyatathionine gamm
634	6	1.8	388	2	S45013	MptI protein - yea
635	6	1.8	389	2	D83139	hypothetical prote
636	6	1.8	390	2	AC3180	agrobacterium viru
637	6	1.8	390	2	A83433	translocator prote
638	6	1.8	390	2	T48524	lysophospholipase-
639	6	1.8	391	2	T35470	probable integral
640	6	1.8	392	2	B86847	cation transporter
641	6	1.8	393	2	D95894	probable hydrolase
642	6	1.8	394	2	AH0490	sugar transport sy
643	6	1.8	395	2	C71219	hypothetical prote
644	6	1.8	395	2	J00430	hypothetical 44.4k
645	6	1.8	397	2	B86663	multidrug-efflux t
646	6	1.8	399	1	F70427	glyniptoleolate sy
647	6	1.8	399	2	A10322	glycine betaine/L-
648	6	1.8	399	2	G86872	galactokinase (EC
649	6	1.8	399	2	T18566	hypothetical prote
650	6	1.8	399	2	C83847	cytochrome c bioge
651	6	1.8	399	2	F83796	multidrug-efflux t
652	6	1.8	400	2	S30382	glycine hydroymet
653	6	1.8	400	2	D75331	hypothetical prote
654	6	1.8	401	1	WZBE81	gene 17 protein -
655	6	1.8	401	2	H83911	hypothetical prote
656	6	1.8	402	2	JE0282	cell division prot
657	6	1.8	403	2	E70618	probable fader7 pro
658	6	1.8	403	2	F75331	ATP-dependent Clp
659	6	1.8	403	2	C97933	hypothetical prote
660	6	1.8	406	2	D64647	conserved hypotet
661	6	1.8	406	2	AC3267	hypothetical prote
662	6	1.8	407	2	T41708	gcp binding protel
663	6	1.8	407	2	JE0113	zinc-finger protel
664	6	1.8	407	2	S62492	hypothetical PMW
665	6	1.8	408	2	T44859	glycosyltransferas
666	6	1.8	408	2	D71147	hypothetical prote
667	6	1.8	408	2	F97304	selenocysteine lya
668	6	1.8	408	2	T39570	probable metal tra
669	6	1.8	409	1	B0A655	virB10 protein - A
670	6	1.8	409	2	T30586	glycosyltransferas
671	6	1.8	409	2	G71936	hypothetical prote
672	6	1.8	409	2	T24138	hypothetical prote
673	6	1.8	410	2	AC3693	large terminase f1
674	6	1.8	412	2	C96816	hypothetical prote
675	6	1.8	412	2	AF3289	transporter, mfs s
676	6	1.8	413	2	EA4120	serine hydroymeth
677	6	1.8	413	2	C90554	hypothetical prote
678	6	1.8	413	2	AC1392	glycine hydroymet
679	6	1.8	413	2	AE1767	glycine hydroymet
680	6	1.8	413	2	G85854	probable transport
681	6	1.8	413	2	E82782	phage-related inte
682	6	1.8	414	1	JQ0106	glycine hydroymet
683	6	1.8	414	2	S75052	hypothetical prote
684	6	1.8	415	1	I40483	glycine hydroymet
685	6	1.8	415	2	S40911	septin CDC11 - yea
686	6	1.8	415	2	H81079	lipoprotein NlpD,

687	6	1.8	415	2	G81864	probable membrane	760	6	1.8	444	2	T25111	hypothetical prote
688	6	1.8	416	2	F90076	hypothetical prote	761	6	1.8	444	2	E90192	DNA repair protein
689	6	1.8	416	2	G64542	glycine hydroxymet	762	6	1.8	445	1	A45111	D-alanine/glycine
690	6	1.8	416	2	T50429	dna polymerase gam	763	6	1.8	445	2	T21744	hypothetical prote
691	6	1.8	416	2	A84975	UDP-N-acetylglucos	764	6	1.8	446	2	S75708	hypothetical prote
692	6	1.8	416	2	H64984	hypothetical 43.4	765	6	1.8	446	2	B70972	hypothetical prote
693	6	1.8	418	2	E91010	probable transport	766	6	1.8	446	2	T39874	hypothetical prote
694	6	1.8	418	2	H86848	hypothetical prote	767	6	1.8	447	2	T12978	hypothetical prote
695	6	1.8	419	2	D97475	probable large ter	768	6	1.8	447	2	G95068	hypothetical prote
696	6	1.8	419	2	C95091	conserved hypotet	769	6	1.8	447	2	G97936	cysteinyI-CRNA syn
697	6	1.8	419	2	G97958	conserved hypotet	770	6	1.8	447	2	T05070	hypothetical prote
698	6	1.8	420	1	S34379	glycine hydroxymet	771	6	1.8	447	2	A39321	hypothetical prote
699	6	1.8	421	1	D64100	glycine hydroxymet	772	6	1.8	448	2	I48128	mucin - rat (fragm
700	6	1.8	421	2	S26246	glutamate/aspartat	773	6	1.8	448	2	S57609	vimentin - Chinese
701	6	1.8	421	2	S26247	glutamate/aspartat	774	6	1.8	449	2	S76839	probable histidine
702	6	1.8	421	2	H69490	formylmethanofuran	775	6	1.8	450	2	A12324	hypothetical prote
703	6	1.8	421	2	H86184	hypothetical prote	776	6	1.8	450	2	B70506	hypothetical prote
704	6	1.8	422	2	C98200	serine hydroxymet	777	6	1.8	451	2	D72422	hypothetical prote
705	6	1.8	422	2	AF3086	probable regulator	778	6	1.8	451	2	A81206	sugar transporter,
706	6	1.8	422	2	T36626	ycdb protein precu	779	6	1.8	451	2	E81781	probable integral
707	6	1.8	423	2	A64844	hypothetical prote	780	6	1.8	453	2	JH0696	plastidin - goldfl
708	6	1.8	423	2	A99787	hypothetical prote	781	6	1.8	453	2	E69755	hypothetical prote
709	6	1.8	423	2	A85647	chloramphenicol re	782	6	1.8	453	2	S39866	outer membrane pro
710	6	1.8	425	1	H69784	hypothetical prote	783	6	1.8	454	2	S39866	hypothetical prote
711	6	1.8	425	2	T18592	hypothetical prote	784	6	1.8	455	1	AD2460	rhodopsin - giant
712	6	1.8	425	2	T41172	hypothetical prote	785	6	1.8	455	1	OOOCG	hypothetical prote
713	6	1.8	425	2	A87631	FMN oxidoreductase	786	6	1.8	455	2	A43950	vimentin - common
714	6	1.8	426	2	C70896	glycine hydroxymet	787	6	1.8	456	2	A60090	peripherin - Afric
715	6	1.8	426	2	D87153	serine hydroxymet	788	6	1.8	457	2	F88493	protein F57B9.9 (f
716	6	1.8	426	2	G83983	C4-dicarboxylate t	789	6	1.8	457	2	I64429	glycerol-3-phospha
717	6	1.8	426	2	H65102	probable tagatose	790	6	1.8	457	2	S18939	UDP-N-acetylglucos
718	6	1.8	426	2	B91130	probable tagatose	791	6	1.8	457	2	AB1426	Grpase homolog lmo
719	6	1.8	426	2	B85975	probable tagatose	792	6	1.8	458	2	AH1799	Grpase homolog lmo
720	6	1.8	426	2	AE0907	cytosine deaminase	793	6	1.8	458	2	A43554	vimentin - African c
721	6	1.8	427	2	S75210	glycine hydroxymet	794	6	1.8	458	2	A43549	vimentin 1 - Afric
722	6	1.8	427	2	F72341	glycine hydroxymet	795	6	1.8	458	2	E82340	probable gluconate
723	6	1.8	427	2	AE2406	serine hydroxymet	796	6	1.8	458	2	G86561	UDP-N-acetylglucos
724	6	1.8	427	2	A71612	translation releas	797	6	1.8	458	2	D72063	hypothetical prote
725	6	1.8	427	2	F64084	3-deoxy-manno-ctu	798	6	1.8	459	2	AD2060	hypothetical prote
726	6	1.8	427	2	F90677	cytosine deaminase	799	6	1.8	460	2	H82088	DNA repair protein
727	6	1.8	427	2	E87669	conserved hypotet	800	6	1.8	460	2	A29329	vimentin - chicken
728	6	1.8	427	2	E72377	conserved hypotet	801	6	1.8	460	2	D72694	hypothetical prote
729	6	1.8	427	2	S22662	cytosine deaminase	802	6	1.8	461	2	T48137	hypothetical prote
730	6	1.8	427	2	B85528	cytosine deaminase	803	6	1.8	461	2	S44733	copper amine oxid
731	6	1.8	427	2	AC1394	human N-acetylgluc	804	6	1.8	462	1	T17310	b0533.4 protein
732	6	1.8	427	2	AE1769	weakly human N-ace	805	6	1.8	462	1	S35534	hypothetical prote
733	6	1.8	428	2	D70343	glycine hydroxymet	806	6	1.8	462	2	I53414	adenovirus E1A enh
734	6	1.8	429	2	AD2720	serine hydroxymet	807	6	1.8	462	2	AF1694	lamin C2 - mouse
735	6	1.8	430	2	AH3420	phage DNA packagin	808	6	1.8	463	1	T34365	hypothetical prote
736	6	1.8	430	2	T26405	hypothetical prote	809	6	1.8	463	2	A34285	desmin - chicken
737	6	1.8	433	2	S76485	hypothetical prote	810	6	1.8	463	2	B43549	NADH dehydrogenase
738	6	1.8	433	2	T01574	indeterminate splik	811	6	1.8	464	1	VEHY	vimentin 4 - Afric
739	6	1.8	434	2	S30334	glycine hydroxymet	812	6	1.8	464	2	A05026	vimentin - golden
740	6	1.8	434	2	AE0226	conserved hypotet	813	6	1.8	464	2	T50955	hypothetical prote
741	6	1.8	435	2	D82955	probable MPS dicar	814	6	1.8	465	2	F70364	hypothetical prote
742	6	1.8	436	2	F75567	serine hydroxymet	815	6	1.8	466	2	A25074	dihydrolipoamide d
743	6	1.8	436	2	A81443	probable transmemb	816	6	1.8	466	2	A43803	vimentin - human
744	6	1.8	436	2	AG0020	cytosine deaminase	817	6	1.8	466	2	S22119	vimentin - mouse
745	6	1.8	437	2	JC4288	preprotein transio	818	6	1.8	466	2	T41125	vimentin - rat
746	6	1.8	437	2	S50006	preprotein transio	819	6	1.8	466	2	T39426	glucose-ubiquitin
747	6	1.8	437	2	JC5115	preprotein transio	820	6	1.8	469	1	DMHU	probable ubiquitin
748	6	1.8	438	2	E55578	hypothetical prote	821	6	1.8	469	2	I52469	desmin - human
749	6	1.8	439	2	B70629	hypothetical prote	822	6	1.8	469	2	A24783	desmin - rat
750	6	1.8	439	2	B44315	cartilage oligomer	823	6	1.8	469	2	A44841	desmin - golden ha
751	6	1.8	440	2	A42136	transcription fact	824	6	1.8	469	2	A54104	low molecular wely
752	6	1.8	440	2	S49765	Tya protein - yeas	825	6	1.8	470	2	H72105	dicarboxylase tran
753	6	1.8	440	2	F69791	conserved hypotet	826	6	1.8	470	2	G86516	dicarboxylase tran
754	6	1.8	440	2	S58302	hypothetical prote	827	6	1.8	472	2	S41720	intermediate filam
755	6	1.8	441	2	T32021	hypothetical prote	828	6	1.8	472	2	F90355	multidrug resistan
756	6	1.8	441	2	C85761	anthranilate synth	829	6	1.8	472	2	B99372	multidrug resistan
757	6	1.8	442	2	D84224	heme synthase (lmp	830	6	1.8	472	2	H70873	probable exported
758	6	1.8	443	2	T35974	probable aminoacyl	831	6	1.8	473	2	I54210	N-acetylglactosam
759	6	1.8	443	2	T37666	26S proteasome reg	832	6	1.8	473	2	A48949	beta-glucosidase,

833	6	1.8	473	2	C86841	hypothetical prote	906	6	1.8	509	2	T07721	hypothetical prote
834	6	1.8	474	2	AC1904	hypothetical prote	907	6	1.8	509	2	AC2217	hypothetical prote
835	6	1.8	475	1	VHNSY	nucleoprotein - So	908	6	1.8	510	2	F75115	co-induced hydroge
836	6	1.8	476	2	T29083	3-isopropylmalate	909	6	1.8	510	2	A87482	conserved hypothet
837	6	1.8	476	2	AE0916	probable membrane	910	6	1.8	510	2	A12689	two component sens
838	6	1.8	479	2	G82114	sigma-54 dependent	911	6	1.8	511	2	A54676	antiquitin - humn
839	6	1.8	479	2	D30411	synapsin IIb--rat	912	6	1.8	511	2	D70944	probable liprt prot
840	6	1.8	479	2	C90457	cytochrome b558/56	913	6	1.8	513	2	D69016	serine--tRNA ligas
841	6	1.8	480	2	G64360	phenylalanine--trn	914	6	1.8	513	2	AB2504	hypothetical prote
842	6	1.8	480	2	T34102	hypothetical prote	915	6	1.8	513	2	D98225	hypothetical prote
843	6	1.8	482	1	BMVMSY	preprotein translo	916	6	1.8	513	2	AC3061	hypothetical prote
844	6	1.8	482	2	T44628	probable transpos	917	6	1.8	514	2	T15944	hypothetical prote
845	6	1.8	483	2	AF2363	hypothetical prote	918	6	1.8	515	2	T30651	hypothetical prote
846	6	1.8	484	2	AG2097	serine/threonine k	919	6	1.8	515	2	B96825	hypothetical prote
847	6	1.8	485	2	I39699	3-isopropylmalate	920	6	1.8	515	2	D97471	hypothetical senso
848	6	1.8	486	2	A98308	atrk protein (U594	921	6	1.8	516	2	A84081	hypothetical prote
849	6	1.8	486	2	AB2975	succinate semialde	922	6	1.8	517	2	T44289	probable methylal
850	6	1.8	486	2	B70539	hypothetical prote	923	6	1.8	518	2	T11289	cytochrome-c oxida
851	6	1.8	487	1	O4RBC6	cytochrome P450 2C	924	6	1.8	520	1	NNEC1	anthranilate synth
852	6	1.8	487	1	O4RBP4	progesterone monoo	925	6	1.8	520	2	D90858	anthranilate synth
853	6	1.8	487	1	S71770	calcium-dependent	926	6	1.8	520	2	A83203	alginate o-acetyl
854	6	1.8	487	2	A26731	cytochrome P450 2C	927	6	1.8	521	2	A86909	hypothetical prote
855	6	1.8	487	2	B91122	hypothetical prote	928	6	1.8	523	2	S39899	hypothetical prote
856	6	1.8	487	2	A85967	hypothetical prote	929	6	1.8	523	2	C95303	conserved hypothet
857	6	1.8	487	2	A64642	conserved hypothet	930	6	1.8	524	1	S76810	probable NADH deny
858	6	1.8	487	2	B71873	hypothetical prote	931	6	1.8	524	2	E81678	glucose-6-phosphat
859	6	1.8	489	2	C65147	hypothetical 53.7	932	6	1.8	524	2	A75588	probable protein k
860	6	1.8	489	2	H91174	probable transport	933	6	1.8	525	2	F71521	glucose-6-phosphat
861	6	1.8	489	2	H86020	hypothetical prote	934	6	1.8	526	2	F86618	probable glucose-6
862	6	1.8	489	2	D98312	hypothetical prote	935	6	1.8	526	2	C72005	glucose-6-P isomer
863	6	1.8	489	2	AF2870	conserved hypothet	936	6	1.8	526	2	B81533	glucose-6-phosphat
864	6	1.8	490	1	G69282	hypothetical prote	937	6	1.8	526	2	S03600	cell surface antig
865	6	1.8	490	2	A25954	cytochrome P450 2C	938	6	1.8	526	2	T08541	hypothetical prote
866	6	1.8	490	2	A32140	steroid 15beta-mon	939	6	1.8	527	2	S64702	cell surface antig
867	6	1.8	490	2	I48162	cytochrome P450 -	940	6	1.8	527	2	A75399	hypothetical prote
868	6	1.8	490	2	I48163	cytochrome P450 II	941	6	1.8	529	2	T16589	chaperonin beta ch
869	6	1.8	490	2	I48189	cytochrome P450 -	942	6	1.8	529	2	E84813	hypothetical prote
870	6	1.8	490	2	I49610	cytochrome P450 -	943	6	1.8	530	2	C82344	phosphoribosylam
871	6	1.8	490	2	I52410	cytochrome P450 II	944	6	1.8	530	2	T06237	probable high affi
872	6	1.8	490	2	A36122	cytochrome P450 2C	945	6	1.8	531	2	A84422	hypothetical prote
873	6	1.8	490	2	H95033	xanthine/uracil pe	946	6	1.8	531	2	AB4444	hypothetical prote
874	6	1.8	490	2	H97904	conserved hypothet	947	6	1.8	532	1	OFPCM	neurofilament trip
875	6	1.8	490	2	A55141	GlcNAc beta-1,4-N-	948	6	1.8	532	2	H83893	two-component sens
876	6	1.8	490	2	AB2335	hypothetical prote	949	6	1.8	532	2	G87912	protein B0205.9 [1
877	6	1.8	491	2	H97501	serine hydroxymeth	950	6	1.8	535	2	D84340	hypothetical prote
878	6	1.8	491	2	S44657	cosmid ZK353 prote	951	6	1.8	536	2	A13544	aldehyde dehydroge
879	6	1.8	491	2	F70699	probable pbpa prot	952	6	1.8	537	2	F97546	hypothetical prote
880	6	1.8	492	2	S75049	hypothetical prote	953	6	1.8	537	2	AB2766	sulfate permease [
881	6	1.8	494	2	A89930	glucose-6-phosphat	954	6	1.8	538	2	T28874	hypothetical prote
882	6	1.8	494	2	I52658	neurofilament-66	955	6	1.8	540	2	G83589	hypothetical prote
883	6	1.8	495	2	F86469	protein F12K21.8	956	6	1.8	541	2	T34850	probable phosphat
884	6	1.8	496	2	S68160	probable RNA bindi	957	6	1.8	541	2	C70789	probable acid--CoA
885	6	1.8	496	2	T04640	hypothetical prote	958	6	1.8	544	2	G69072	conserved hypothet
886	6	1.8	499	2	F84149	transposase (25) B	959	6	1.8	544	2	T17547	proline-rich prote
887	6	1.8	499	2	T39186	glucose-6-phosphat	960	6	1.8	544	2	AE3375	methionyl-tRNA syn
888	6	1.8	501	2	B71790	ADP,ATP carrier pr	961	6	1.8	545	2	B44054	orf2 protein - Jun
889	6	1.8	501	2	B97790	ADP,ATP carrier pr	962	6	1.8	546	2	B97645	Integral membrane
890	6	1.8	501	2	D87613	pilus assembly pro	963	6	1.8	551	2	G95099	DNA polymerase III
891	6	1.8	502	2	T48595	protoporphyrinogen	964	6	1.8	551	2	A97968	DNA-directed DNA P
892	6	1.8	502	2	S10505	nicotinic acetylch	965	6	1.8	552	2	F69817	conserved hypothet
893	6	1.8	503	2	C69277	2-isopropylmalate	966	6	1.8	553	2	C75318	hypothetical prote
894	6	1.8	503	2	AC0062	conserved hypothet	967	6	1.8	555	1	S24061	hypothetical fact
895	6	1.8	504	2	I53868	alpha-Internexin -	968	6	1.8	555	1	I53869	zinc finger protel
896	6	1.8	505	2	C82216	probable fumarate	969	6	1.8	555	2	T45351	ferredoxin [import
897	6	1.8	505	2	A41023	alpha-Internexin -	970	6	1.8	557	2	AE0204	methyl--acceptin c
898	6	1.8	506	2	B84339	hypothetical prote	971	6	1.8	558	2	B99494	dihydroxy--acid deb
899	6	1.8	506	2	E70200	hypothetical prote	972	6	1.8	558	2	F64235	Na+ ATPase chain J
900	6	1.8	506	2	T35261	probable metallope	973	6	1.8	560	2	T19622	hypothetical prote
901	6	1.8	507	2	A83105	probable fumarate	974	6	1.8	560	2	D84205	hypothetical prote
902	6	1.8	508	1	JC5713	25-hydroxyvitamin	975	6	1.8	561	2	AG1861	hypothetical prote
903	6	1.8	508	2	C87564	cell division prot	976	6	1.8	562	2	T32581	hypothetical prote
904	6	1.8	508	2	T37224	hypothetical prote	977	6	1.8	563	2	E70752	probable dead prot
905	6	1.8	509	1	TVHAST	protein-tyrosine k	978	6	1.8	564	2	T12550	hypothetical prote

979 6 1.8 565 2 B70652 probable cy5g prot
980 6 1.8 565 2 S73707 Na(+) translocatin
981 6 1.8 567 2 F87594 conserved hypothe
982 6 1.8 568 2 A89598 acetyl-CoA synthe
983 6 1.8 569 2 S64957 aspergillopepsin I
984 6 1.8 570 2 T01399 hypothetical prote
985 6 1.8 570 2 G72595 hypothetical prote
986 6 1.8 571 1 S30253 GABA transport pro
987 6 1.8 572 1 VEHULC lamin C - human
988 6 1.8 572 2 VER749 hypothetical prote
989 6 1.8 573 2 T29880 hypothetical prote
990 6 1.8 573 2 A13332 urease alpha chain
991 6 1.8 574 2 S04333 lamin C - mouse
992 6 1.8 574 2 C82301 endoglucanase rela
993 6 1.8 574 2 T51799 CLU1-like protein
994 6 1.8 576 2 AB0863 L-fuculose isomera
995 6 1.8 577 1 DNBYPA polyadenylate-bind
996 6 1.8 579 2 AF1788 DNA polymerase III
997 6 1.8 579 2 AG1412 DNA polymerase III
998 6 1.8 580 2 T30583 probable peptide S
999 6 1.8 581 2 T36267 probable glutamyl-
1000 6 1.8 581 2 T05550 hypothetical prote

ALIGNMENTS

RESULT 1
C65015
hypothetical protein b2412 - Escherichia coli (strain K-12)
C:/Species: Escherichia coli
C:/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 08-Oct-1999
C:/Accession: C65015
R:/Blatnet, F.R.: Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:/Title: The complete genome sequence of Escherichia coli K-12.
A:/Reference number: A64720, MUID:97426617
A:/Accession: C65015
A:/Status: preliminary; nucleic acid sequence not shown; translation not shown
A:/Molecule type: DNA
A:/Residues: 1-328 <BLAT>
A:/Cross-references: GB:AE000329; GB:U00096; NID:q2367137; PID:NAC75465.1; PID:g1788752;
A:/Experimental source: strain K-12, substrain MG1655

Query Match 69.2%; Score 227; DB 2; Length 328;
Best Local Similarity 99.7%; Pred. No. 6.9e-225;
Matches 327; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMODLLILIIIVGAIATIALLVHGFWTSKRERSSMFRDRPLKRMKSKRDDSDYDEVEDD 60
DB 1 MMODLLILIIIVGAIATIALLVHGFWTSKRERSSMFRDRPLKRMKSKRDDSDYDEVEDD 60
QY 61 EGVGEVVRVHRVNHAPANAQEHAAARSPQHOYOPPYASAPROPOVQOPEAQPPOHAP 120
DB 61 EGVGEVVRVHRVNHAPANAQEHAAARSPQHOYOPPYASAPROPOVQOPEAQPPOHAP 120
QY 121 PAQVQOAPVQOPEOPLQOQVSPQVAPAPQVYHSAPOPAQOAFQPAEPVAPAPPEPVAE 180
DB 121 PAQVQOAPVQOPEOPLQOQVSPQVAPAPQVYHSAPOPAQOAFQPAEPVAPAPPEPVAE 180
QY 181 PAPVMPKPKRKEAVITIMNVAAHSGELNGBALINSTQOAGFTFGDMNIIYHRHLSPDGSGP 240
DB 181 PAPVMPKPKRKEAVITIMNVAAHSGELNGBALINSTQOAGFTFGDMNIIYHRHLSPDGSGP 240
QY 241 ALFSLANMKPGTFDEPMKDFTPGVTIFMOVPSYGDDELONFKMLQSNQHTADEVGGV 300
DB 241 ALFSLANMKPGTFDEPMKDFTPGVTIFMOVPSYGDDELONFKMLQSNQHTADEVGGV 300
QY 301 LDDQRMMTPOKLREYODIIRREYKDANA 328
DB 301 LDDQRMMTPOKLREYODIIRREYKDANA 328

RESULT 2
D91039
cell division protein involved in FtsZ ring [imported] - Escherichia coli (strain O15
C:/Species: Escherichia coli
C:/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18-Jul-2001
C:/Accession: D91039
R:/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shibata, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and 9
A:/Reference number: A99629, MUID:2116231; PMID:11258796
A:/Accession: D91039
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-332 <HAY>
A:/Cross-references: GB:BA000007; PIDN:BA036707.1; PID:g13362754; GSPDB:GN00154
A:/Experimental source: strain O157:H7, substrain RIMD 0509952
A:/Gene: ECS3284

Query Match 36.3%; Score 119; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 5.9e-114;
Matches 119; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMODLLILIIIVGAIATIALLVHGFWTSKRERSSMFRDRPLKRMKSKRDDSDYDEVEDD 60
DB 1 MMODLLILIIIVGAIATIALLVHGFWTSKRERSSMFRDRPLKRMKSKRDDSDYDEVEDD 60
QY 61 EGVGEVVRVHRVNHAPANAQEHAAARSPQHOYOPPYASAPROPOVQOPEAQPPOHAP 119
DB 61 EGVGEVVRVHRVNHAPANAQEHAAARSPQHOYOPPYASAPROPOVQOPEAQPPOHAP 119

RESULT 3
G85883
cell division protein involved in FtsZ ring [imported] - Escherichia coli (strain O15
C:/Species: Escherichia coli
C:/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:/Accession: G85883
R:/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
hiller, L.; Grobeck, E.J.; Davis, N.W.; Llin, A.; Dimalanta, E.; Potlamsists, K.; Apoda
Nature 409, 529-533, 2001
A:/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:/Reference number: A85480; MUID:21074935; PMID:11206551
A:/Accession: G85883
A:/Status: preliminary
A:/Molecule type: DNA
A:/Residues: 1-328 <STO>
A:/Cross-references: GB:AE005174; NID:g12516785; PIDN:AG57531.1; GSPDB:GN00145; UMGCP:
A:/Experimental source: strain O157:H7, substrain EDL933
C:/Genetics:
A:/Gene: zipa

Query Match 35.7%; Score 117; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 6.6e-112;
Matches 117; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMODLLILIIIVGAIATIALLVHGFWTSKRERSSMFRDRPLKRMKSKRDDSDYDEVEDD 60
DB 1 MMODLLILIIIVGAIATIALLVHGFWTSKRERSSMFRDRPLKRMKSKRDDSDYDEVEDD 60
QY 61 EGVGEVVRVHRVNHAPANAQEHAAARSPQHOYOPPYASAPROPOVQOPEAQPPOH 117
DB 61 EGVGEVVRVHRVNHAPANAQEHAAARSPQHOYOPPYASAPROPOVQOPEAQPPOH 117

RESULT 4
AB0810
cell division protein [imported] - Salmonella enterica subsp. enterica serovar Typh

C:Species: *Salmonella enterica* subsp. *enterica* serovar *Typh*
A:Note: This species has also been called *Salmonella typhi*
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AB0810
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar
A:Reference number: AB0502; PMID:11677608
A:Accession: AB0810
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-328 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD07660.1; PID:g16503647; GSPDB:GN00176
C:Genetics:
Gene: SRY2664

Query Match 16.5%; Score 54; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 3.4e-47;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MMDLRLLIIVGAIATALLVHGFTSRKRSRSMFRDRLKMKSRDDSDYD 54
DB 1 MMDLRLLIIVGAIATALLVHGFTSRKRSRSMFRDRLKMKSRDDSDYD 54

RESULT 5
AG0363
probable cell division protein YPO2990 [Imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AG0363
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibbitt, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11. M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AG0363
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-328 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC92234.1; PID:g15980946; GSPDB:GN00175
C:Genetics:
Gene: YPO2990

Query Match 3.4%; Score 11; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.005;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 242 LFSLANVVKPG 252
DB 239 LFSLANVVKPG 249

RESULT 6
T22308
hypothetical protein F46F2.3 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T22308
R:Thomas, K.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19545
A:Accession: T22308
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-137 <WIL>
A:Cross-references: EMBL:Z69903; PIDN:CAA93772.1; GSPDB:GN00026; CESP:F46F2.3

A:Experimental source: clone F46F2
C:Genetics:
A:Gene: CESP:F46F2.3
A:Map position: X
A:Introns: 76/3

Query Match 2.7%; Score 9; DB 2; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 126 QQPAYQPOP 134
DB 67 QQPAYQPOP 75

RESULT 7
D84353
hypothetical protein Vng2029h [Imported] - *Halobacterium* sp. NRC-1
C:Species: *Halobacterium* sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84353
R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Laeky ; Leibauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja Jung, K.H.; Alam, M.; Freltas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; A:Title: Genome sequence of *Halobacterium* species NRC-1.
A:Reference number: A84160; MUID:20504483
A:Accession: D84353
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-130 <STO>
A:Cross-references: GB:AE004437; NID:g10581457; PIDN:AG20192.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNG2029H

Query Match 2.4%; Score 8; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 PAEPVAP 173
DB 74 PAEPVAP 81

RESULT 8
S37920
MBR1 protein precursor - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein YKL093w; protein YKL440
C:Species: *Saccharomyces cerevisiae*
C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 21-Jul-2000
C:Accession: S37920; S39093; S37919; S42004; S45577; S27427; S39116
R:Cheret, G.; Fukuhara, H.; Bolotin-Fukuhara, M.; Daignan-Fornier, B.; Pallier, C.; P yeast 9, 1149-1155, 1993
A:Title: DNA sequence analysis of a 17 kb fragment of yeast chromosome XI physically protein kinases.
A:Reference number: S39084; MUID:94078677
A:Accession: S39093
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-208 <PAL>
A:Cross-references: EMBL:X71133; NID:g431205; PIDN:CAA50464.1; PID:g450764
A:Experimental source: strain S288C

DB 16 PEPVAPPA 23

RESULT 12

B86015

probable transport yjhs [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: B86015
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.D.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Llin, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: AB5480; MUID:21074935; PMID:11206551
A:Accession: B86015
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-419 <STO>
C:Cross-references: GB:AE005174; NID:g12518132; PIDN:AA658582.1; GSPDB:GN00145; UNGP:248
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yjhs
C:Superfamily: hypothetical protein b2322

Query Match 2.4%; Score 8; DB 2; Length 419;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 175 PEPVAPPA 182
DB 16 PEPVAPPA 23

RESULT 13

G86773

citrate (pro-3S)-lyase (EC 4.1.3.6) alpha chain [imported] - Lactococcus lactis subsp. 1
N:Alternate names: citrate lyase alpha chain
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: G86773
R:Boltin, A.; Wincker, P.; Mueger, S.; Jallion, O.; Malarme, K.; Weissbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
A:Reference number: AB6625; MUID:21235186; PMID:1137471
A:Accession: G86773
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-512 <STO>
A:Cross-references: GB:AE005176; PID:g12724158; PIDN:AAK05289.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: citF
C:Superfamily: Escherichia citrate (pro-3S)-lyase alpha chain
C:Keywords: carbon-carbon lyase; oxo-acid-lyase

Query Match 2.4%; Score 8; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 318 DIREVKD 325
DB 505 DIREVKD 512

RESULT 14

B97566

hypothetical protein AGR_C_3142 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: B97566
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,

A.; Liu, F.; Mollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lapps, C.; Markelz,
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium
A:Reference number: A97359; PMID:11743194
A:Accession: B97566
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-912 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK87483.1; PID:g15156806; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_3142
A:Map position: circular chromosome

Query Match 2.4%; Score 8; DB 2; Length 912;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 146 VAPAPQPV 153
DB 350 VAPAPQPV 357

RESULT 15

AH2786

conserved hypothetical protein Atu1710 [imported] - Agrobacterium tumefaciens (strain
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AH2786
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuyavin, T.; Levy, R.; Li, M.; McCl
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AH2786
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1008 <KUR>
A:Cross-references: GB:AE008688; PIDN:AAI42710.1; PID:g17740147; GSPDB:GN00186
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu1710
A:Map position: circular chromosome

Query Match 2.4%; Score 8; DB 2; Length 1008;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 146 VAPAPQPV 153
DB 446 VAPAPQPV 453

Search completed: September 25, 2002, 09:53:30
Job time: 159 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 25, 2002, 09:52:56 ; Search time 13.47 Seconds
(without alignments)
942.837 Million cell updates/sec

Title: US-09-184-826-2
328
Perfect score: 1 MMQDLRLILIVGAIATIAL.....TPQKLRKYQDIIRVKDANA 328
Sequence: 1 MMQDLRLILIVGAIATIAL.....TPQKLRKYQDIIRVKDANA 328

Scoring table:
OLIGO
Gap 60.0 , Gapext 60.0
Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	328	100.0	328	1 ZIPA_ECOLI	P77173 escherichia
2	54	16.5	328	1 ZIPA_SALTY	P55694 salmonella
3	11	3.4	328	1 ZIPA_YERPE	P58492 yersinia pe
4	8	2.4	339	1 MBRL_YEAST	P23493 saccharomyc
5	8	2.4	419	1 YHNS_ECOLI	P37621 escherichia
6	8	2.4	541	1 BCHB_CHLOI	Q916x5 chloroflexu
7	8	2.4	591	1 ALU8_HUMAN	P39195 homo sapien
8	8	2.4	593	1 ALU7_HUMAN	P39194 homo sapien
9	7	2.1	49	1 LHA3_ECTHA	P80107 ecctothiorho
10	7	2.1	178	1 RL17_LEPIN	Q9x08 leprospira
11	7	2.1	206	1 RS3A_HALNI	Q9h45 halobacteri
12	7	2.1	255	1 GRPS_MYXXA	P95333 myxococcus
13	7	2.1	277	1 TRT1_HUMAN	P13805 homo sapien
14	7	2.1	288	1 ALF_MYCGE	P47269 mycoplasma
15	7	2.1	289	1 ZIPA_PSEAE	Q91315 pseudomonas
16	7	2.1	291	1 ZIPA_VIBCH	Q9kcd2 vibrio chol
17	7	2.1	323	1 KHSE_PPRHO	Q9k814 pyrococcus
18	7	2.1	328	1 HEMB_BACCH	Q9k892 bacillus ha
19	7	2.1	330	1 RIL_HUMAN	P50479 homo sapien
20	7	2.1	362	1 CD44_CRIGR	P20844 cricetulus
21	7	2.1	401	1 CASP_HUMAN	O75718 homo sapien
22	7	2.1	431	1 CD44_MESAU	O60522 m cd44 anti
23	7	2.1	463	1 NU4M_STRPU	P15551 strongyloce
24	7	2.1	466	1 ZIC3_MOUSE	Q62521 mus musculi
25	7	2.1	467	1 ZIC3_HUMAN	O60481 mus musculi
26	7	2.1	482	1 TRPE_SPIAU	P21690 spiriochaeta
27	7	2.1	487	1 TRPD_ECOLI	P39414 escherichia
28	7	2.1	500	1 NU4C_OENHO	P58419 oenothera h
29	7	2.1	502	1 YH60_MYCTU	O06751 mycobacteri
30	7	2.1	503	1 CD44_RAT	P26051 rattus norv
31	7	2.1	516	1 UDPG_SCHPO	P78811 schizosacch
32	7	2.1	511	1 KLFB_MOUSE	O9ef4 mus musculu
33	7	2.1	512	1 KLFB_HUMAN	O14901 homo sapien

34	7	2.1	579	1 SYN3_RAT	O70441 rattus norv
35	7	2.1	583	1 FTS2_AGRU	O30992 agrobacteri
36	7	2.1	585	1 ALU5_HUMAN	P39192 homo sapien
37	7	2.1	655	1 CD44_MOUSE	P15379 mus musculi
38	7	2.1	676	1 VGP_EBOIC	O66810 ebola virus
39	7	2.1	676	1 VGP_EBOSB	O66814 ebola virus
40	7	2.1	676	1 VGP_EBOSM	O66798 ebola virus
41	7	2.1	677	1 VGP_EBORS	O66799 ebola virus
42	7	2.1	677	1 VGP_EBORS	O66799 ebola virus
43	7	2.1	1006	1 EPB6_HUMAN	O89853 ebola virus
44	7	2.1	1014	1 EPB6_MOUSE	O15197 homo sapien
45	7	2.1	1018	1 HMB1_MYCPN	O08644 mus musculi
46	7	2.1	1073	1 YPD4_YEAST	O50365 mycoplasma
47	7	2.1	1242	1 TBP7_CAEEL	P43564 saccharomyc
48	7	2.1	1362	1 BRD4_HUMAN	P54816 caenorhabdi
49	7	2.1	1553	1 TP2A_CHICK	O60885 homo sapien
50	7	2.1	1782	1 VIT_BOMO	O42130 gallus galli
51	7	2.1	6359	1 BACC_BACLI	O27309 bombyx mori
52	6	1.8	41	1 PSNJ_CHLYU	O68008 b bacitraci
53	6	1.8	42	1 PSNJ_NEPOL	P56340 chlorella v
54	6	1.8	79	1 OAG3_SALTY	O9kx28 nephroselm
55	6	1.8	82	1 HFO_CAUCR	P58651 salmonella
56	6	1.8	88	1 RS16_BACST	O9a7h8 caulobacter
57	6	1.8	92	1 RLG_EMTHT	P81290 bacillus st
58	6	1.8	93	1 YPB3_YEAST	O15595 entamoeba h
59	6	1.8	95	1 FER_MARPO	O14464 saccharomyc
60	6	1.8	98	1 CYTA_BOVIN	P09735 marchantia
61	6	1.8	98	1 YAM3_YEAST	P80416 bos taurus
62	6	1.8	110	1 YC27_ARCFU	P39559 saccharomyc
63	6	1.8	111	1 RL22_CHLTR	O29041 archaeoglob
64	6	1.8	121	1 AMEL_ORNAN	O84528 chlamydia t
65	6	1.8	121	1 FLIO_ECOLI	O97646 ornithorhyn
66	6	1.8	122	1 BCGF_HUMAN	P22586 escherichia
67	6	1.8	124	1 CLP2_DROMI	O31165 spiroplasma
68	6	1.8	126	1 CLP2_DROMI	P20931 homo sapien
69	6	1.8	126	1 SYN2_MOUSE	P91629 dirosophila
70	6	1.8	128	1 C562_ECOLI	O64332 mus musculi
71	6	1.8	131	1 PRO5_ARATH	P00192 escherichia
72	6	1.8	133	1 CLP1_DROMI	O91663 arabidopsis
73	6	1.8	138	1 FLAF_METUA	P33460 caprine art
74	6	1.8	139	1 LSAB_CERS1	P91627 dirosophila
75	6	1.8	141	1 EIBS_ADE04	O58307 methanococc
76	6	1.8	142	1 IF1A_RABIT	P78735 ceratotheri
77	6	1.8	144	1 R12A_ARATH	P10406 human adeno
78	6	1.8	144	1 RL28_TRYCR	P47814 oryctolagus
79	6	1.8	146	1 RS9_AQUAE	O9a9p1 arabidopsis
80	6	1.8	147	1 ALL5_HEVBR	O00822 trypanosoma
81	6	1.8	150	1 NU6M_CANPA	O67723 aquifex aeo
82	6	1.8	155	1 COAD_HAELN	O39667 hevea brasl
83	6	1.8	156	1 COAD_HELPU	P48925 candida par
84	6	1.8	157	1 COAD_HELPJ	P48405 haemophilus
85	6	1.8	157	1 COAD_HELPJ	O9a7e4 helicobacte
86	6	1.8	158	1 COAD_CAMJE	O26010 helicobacte
87	6	1.8	158	1 COAD_CAMJE	O9p0f2 campylobact
88	6	1.8	159	1 COAD_ECOLI	O9cld4 pasteurella
89	6	1.8	159	1 COAD_ECOLI	P23875 escherichia
90	6	1.8	159	1 COAD_PSEAE	O9xc89 pseudomonas
91	6	1.8	160	1 COFE_BAGSU	P23761 bacillus su
92	6	1.8	161	1 COAD_AQUAE	O66614 aquifex aeo
93	6	1.8	161	1 COAD_SERNA	O9a980 serratia ma
94	6	1.8	161	1 GLB9_CHITH	P23223 chironomus
95	6	1.8	161	1 GLB9_CHITH	P12548 chironomus
96	6	1.8	161	1 GLB9_CHITH	P12592 chironomus
97	6	1.8	161	1 GLB9_CHITH	P12592 chironomus
98	6	1.8	161	1 GLB9_CHITH	P12549 chironomus
99	6	1.8	161	1 GLB9_CHITH	O23763 chironomus
100	6	1.8	161	1 GLB1_CHITH	P18966 chironomus
101	6	1.8	161	1 GLB1_CHITH	O23762 chironomus
102	6	1.8	162	1 COAD_XYLFH	O9ep98 xyella fas
103	6	1.8	162	1 COAD_XYLFH	O10795 mycobacteri
104	6	1.8	163	1 COAD_CAUCR	P58103 caulobacter
105	6	1.8	163	1 GLB2_CHITH	O23761 chironomus
106	6	1.8	163	1 GLB2_CHITH	O23761 chironomus

107	6	1.8	163	1	GLB2_CHTP	P29245	chironomus	180	6	1.8	298	1	REG5_DROME	Q94913	drosophila
108	6	1.8	164	1	COAD_VIBCH	Q9KVC4	vibrio chol	181	6	1.8	298	1	STX2_CAEEL	Q20574	caenorhabd1
109	6	1.8	165	1	COAD_BUCAI	P57643	buchnera ap	182	6	1.8	301	1	MURB_BACDH	Q9K911	baicillus ha
110	6	1.8	165	1	COAD_BUCAP	Q9Z613	buchnera ap	183	6	1.8	301	1	YW77_MYCTU	Q50687	mycobacter1
111	6	1.8	165	1	SSB_PSEAE	P40947	pseudomonas	184	6	1.8	302	1	HSLO_NEITMA	Q9JX68	neisseria m
112	6	1.8	169	1	COAD_CHRVI	P71154	chromatium	185	6	1.8	302	1	HSLO_NEITB	Q9JX68	neisseria m
113	6	1.8	172	1	Y21B_MERJA	P81222	methanococ	186	6	1.8	303	1	BNK_DROME	Q9JX68	neisseria m
114	6	1.8	176	1	22P2_RAT	P22283	rattus norv	187	6	1.8	303	1	MAGA_XENLA	P40794	xenopus lae
115	6	1.8	178	1	COAD_ZYMO	Q9RME4	zymomonas m	188	6	1.8	305	1	HEM3_AERPE	Q9Y910	drosophila
116	6	1.8	179	1	APT_HELPJ	Q9Z149	helicobacte	189	6	1.8	307	1	DMPB_PSESP	P17362	psaeronym p
117	6	1.8	180	1	CHI9_DROSU	C25226	helicobacte	190	6	1.8	307	1	MENA_SYNY3	P73362	synchocyst
118	6	1.8	181	1	APT_DROPS	P13428	drosophila	191	6	1.8	307	1	NAH1_PSEPU	P08127	psaeronym p
119	6	1.8	181	1	OLED_HELAN	P54363	drosophila	192	6	1.8	307	1	XYE2_PSEPU	P08127	psaeronym p
120	6	1.8	181	1	NUSE_BOBUB	O51335	bellantus	193	6	1.8	309	1	TUS_ECO57	P08127	psaeronym p
121	6	1.8	184	1	NUSE_BOBUB	O51335	bellantus	194	6	1.8	309	1	TUS_ECO57	P08127	psaeronym p
122	6	1.8	185	1	NU6M_SARGL	O63849	sarcophyton	195	6	1.8	309	1	TUS_SALTY	P08127	psaeronym p
123	6	1.8	185	1	YCXB_BACSU	O08793	baicillus su	196	6	1.8	310	1	TUS_KLEPO	O52714	schizosacch
124	6	1.8	187	1	RPOE_LACIA	O52439	lactococcus	197	6	1.8	310	1	Y497_MYCTU	O11162	mycobacter1
125	6	1.8	193	1	BPA2_PSEF1	O9P184	chlamydia m	198	6	1.8	313	1	B3GT_DROME	Q94913	drosophila
126	6	1.8	193	1	Y274_CHLMU	P56187	corynebacte	199	6	1.8	314	1	IKBA_PIG	Q08353	sus scrofa
127	6	1.8	195	1	COAE_CORGL	P75685	escherichia	200	6	1.8	315	1	ATNB_ARTSA	P25169	artemia sal
128	6	1.8	197	1	YKGB_ECOLI	Q28462	monodelphis	201	6	1.8	315	1	SECF_SYNY3	O55611	synchocyst
129	6	1.8	202	1	AMEL_MONDO	Q47498	metridium s	202	6	1.8	319	1	URED_SYNPV	O87399	synchocyst
130	6	1.8	202	1	NU6M_METSE	O91915	odontesthes	203	6	1.8	320	1	HXA4_HUMAN	O00056	homo sapien
131	6	1.8	204	1	SOMA_ODOAR	P17664	chimpanzee	204	6	1.8	321	1	AOC3_RAT	O08390	rattus norv
132	6	1.8	205	1	NEF_SIVC2	P44286	haemophilus	205	6	1.8	322	1	SLP1_DROME	P32030	drosophila
133	6	1.8	209	1	PROO_HAEIN	P33191	solanium tub	206	6	1.8	323	1	NU1M_XENLA	P03690	xenopus lae
134	6	1.8	211	1	TUB8_SOLTU	O04620	plasmodium	207	6	1.8	323	1	ZIPA_PASMU	Q9C8C8	pasteurella
135	6	1.8	213	1	OS24_PLABA	P49546	odontella s	208	6	1.8	324	1	KDGB_BACSU	P50845	baicillus su
136	6	1.8	215	1	RK4_ODOSI	O95716	homo sapien	209	6	1.8	326	1	RP44_YEAST	P46669	saccharomyc
137	6	1.8	219	1	RBJD_HUMAN	O43709	homo sapien	210	6	1.8	327	1	DPEF_HAEIN	P45094	haemophilus
138	6	1.8	220	1	MTXN_HUMAN	P19972	p salt-medi	211	6	1.8	327	1	GRNR_RAT	P30969	rattus norv
139	6	1.8	222	1	TOXK_PICPA	Q21693	caenorhabd1	212	6	1.8	328	1	HXDI_HUMAN	Q94220	homo sapien
140	6	1.8	228	1	IFE2_CAEEL	Q11115	caenorhabd1	213	6	1.8	328	1	P2Y6_HUMAN	P44113	haemophilus
141	6	1.8	230	1	YX09_CAEEL	P29286	bradyrhizob	214	6	1.8	329	1	ZIPA_HAEIN	P78974	schizosacch
142	6	1.8	237	1	FIXK_BRAJA	P50731	baicillus su	215	6	1.8	334	1	HEM2_SCHPO	P37313	escherichia
143	6	1.8	240	1	YPBE_BACSU	P48672	carassius a	216	6	1.8	336	1	GLK_XYLEA	P46367	caenorhabd1
144	6	1.8	243	1	VIM2_CARAU	P03206	epstein-bar	217	6	1.8	337	1	GLK_XYLEA	Q9PE94	xyella fas
145	6	1.8	245	1	BZLF_EBV	P43162	gracilaria	218	6	1.8	343	1	HRCA_BACSH	O69656	baicillus sp
146	6	1.8	250	1	TPIS_GRAVE	P43162	streptomyces	219	6	1.8	346	1	CHEB_BACDH	P49885	gallus gall
147	6	1.8	251	1	YMP3_STRCO	P15514	homo sapien	220	6	1.8	353	1	MLIA_CHICK	P26524	azospirillum
148	6	1.8	252	1	AMPR_HUMAN	P32442	homo sapien	221	6	1.8	355	1	TRPD_AZOB	P52129	escherichia
149	6	1.8	253	1	MOXI_MOUSE	O9Y185	aeropyrum p	222	6	1.8	357	1	FEUN_ECOLI	P70618	rattus norv
150	6	1.8	254	1	RS4E_AERPE	O06916	myxococcus	223	6	1.8	360	1	MK14_RAT	Q03180	saccharomyc
151	6	1.8	257	1	GUFA_MYXXA	P17743	haemophilus	224	6	1.8	361	1	PIR3_YEAST	P10100	escherichia
152	6	1.8	258	1	T2C2_HAEIN	P01881	mus musculu	225	6	1.8	362	1	RLPA_ECOLI	O00292	homo sapien
153	6	1.8	263	1	PFLA_STRMU	O68575	streptococc	226	6	1.8	366	1	TGF4_HUMAN	P30325	lymantria d
154	6	1.8	266	1	NIEK_KLEPN	O08534	klebsiella	227	6	1.8	373	1	Y007_METUA	Q9P325	chlamydia m
155	6	1.8	269	1	T2S1_STRFT	O52512	streptomyces	228	6	1.8	376	1	GUNK_FUSOX	P45699	fusarium ox
156	6	1.8	272	1	THIN_BACSU	P39593	baicillus su	229	6	1.8	377	1	VIBX_AGRF5	P09783	agrobacter1
157	6	1.8	273	1	SCF_HUMAN	P21583	homo sapien	230	6	1.8	378	1	Y066_NPVLD	P17800	agrobacter1
158	6	1.8	274	1	P30_MYCPN	P02423	mus musculu	231	6	1.8	377	1	VIBX_AGRF5	P05559	agrobacter1
159	6	1.8	275	1	VIME_PIG	P50429	sus scrofa	232	6	1.8	377	1	VIBX_AGRF5	P05559	agrobacter1
160	6	1.8	285	1	ARSB_MOUSE	O9CE87	lactococcus	233	6	1.8	378	1	CPCE_RABIT	P11372	oryctolagus
161	6	1.8	286	1	AROE_LACIA	P22566	paracoccus	234	6	1.8	379	1	NLPD_ECOLI	P33648	escherichia
162	6	1.8	287	1	MAUI_PARDE	P35219	homo sapien	235	6	1.8	381	1	MAGA_HAEIN	P44537	haemophilus
163	6	1.8	289	1	CAH8_HUMAN	P52170	xanthomonas	236	6	1.8	385	1	CYB_STRPU	P15547	strongyloce
164	6	1.8	290	1	BLAI_XANMA	P28651	mus musculu	237	6	1.8	386	1	CRFY_ERWHE	O01331	erythrina her
165	6	1.8	290	1	CAH8_MOUSE	O9P123	campylobact	238	6	1.8	391	1	HERP_HUMAN	Q01501	homo sapien
166	6	1.8	294	1	KHSE_CAMJE	P44325	haemophilus	239	6	1.8	391	1	HERP_HUMAN	Q01501	homo sapien
167	6	1.8	294	1	CPMN_STRHY	O48609	drosophila	240	6	1.8	393	1	TCR7_VIBAN	P51563	vibrio angu
168	6	1.8	294	1	MTAL_SOREQ	O13595	streptomyces	241	6	1.8	395	1	Y144_STRFR	P20188	streptomyc
169	6	1.8	295	1	TF_MOUSE	P20352	mus musculu	242	6	1.8	396	1	A2BP_MOUSE	Q9J143	mus musculu
170	6	1.8	295	1	TF_MOUSE	P20352	mus musculu	243	6	1.8	397	1	A2BP_MOUSE	Q9J143	mus musculu
171	6	1.8	297	1	TF_MOUSE	P20352	mus musculu	244	6	1.8	399	1	GAU1_LACIA	Q947d7	lactococcus
172	6	1.8	297	1	TF_MOUSE	P20352	mus musculu	245	6	1.8	399	1	GAU1_LACIA	Q947d7	lactococcus
173	6	1.8	297	1	TF_MOUSE	P20352	mus musculu	246	6	1.8	401	1	UL43_HSVB8	P28959	equine herp
174	6	1.8	297	1	TF_MOUSE	P20352	mus musculu	247	6	1.8	406	1	ISDF_HELPY	O25664	h ispd/ispf
175	6	1.8	297	1	TF_MOUSE	P20352	mus musculu	248	6	1.8	407	1	YAR1_SCHPO	Q09842	schizosacch
176	6	1.8	297	1	TF_MOUSE	P20352	mus musculu	249	6	1.8	407	1	YAR1_SCHPO	Q09842	schizosacch
177	6	1.8	297	1	TF_MOUSE	P20352	mus musculu	250	6	1.8	407	1	YAR1_SCHPO	Q09842	schizosacch
178	6	1.8	297	1	TF_MOUSE	P20352	mus musculu	251	6	1.8	407	1	YAR1_SCHPO	Q09842	schizosacch
179	6	1.8	297	1	TF_MOUSE	P20352	mus musculu	252	6	1.8	407	1	YAR1_SCHPO	Q09842	schizosacch

253	6	1.8	409	1	ISDF_HELPD	Q92ml9 h ispd/ispt	326	6	1.8	473	1	BGBL_MTCBI	P38645 microbispor
254	6	1.8	413	1	GLYA_BACHD	Q9k6g4 bacillus ha	327	6	1.8	475	1	NCAP_SYN	P10500 sonchus yel
255	6	1.8	415	1	CC11_YEAST	P32458 saccharomyc	328	6	1.8	476	1	RMOC_SALTY	Q916m7 salmonella
256	6	1.8	415	1	GLYA_BACSU	P39148 bacillus su	329	6	1.8	479	1	CB809_SULISO	P58029 metholobus
257	6	1.8	416	1	ATRY_TRYCR	P33447 trypanosoma	330	6	1.8	480	1	SYFA_METJA	Q57911 metnococc
258	6	1.8	416	1	GLYA_HELPD	P56089 helicobacte	331	6	1.8	482	1	K2C8_RAT	Q10758 rattus norv
259	6	1.8	416	1	MURA_BUCAL	P57466 buchiera ap	332	6	1.8	482	1	SECT_MYCA	P10250 mycoplasma
260	6	1.8	416	1	YEID_ECOLI	P33021 escherichia	333	6	1.8	485	1	LEU2_ACTT1	Q44427 actinoplan
261	6	1.8	420	1	GLYA_ACTAC	P34894 pasteurella	334	6	1.8	485	1	SR54_SYN7	Q53111 synchococc
262	6	1.8	420	1	GLYA_PASMU	P57830 actinobacill	335	6	1.8	487	1	CPCA_RABIT	P1371 oryctolagus
263	6	1.8	421	1	GLTT_BACST	P24944 bacillus ca	336	6	1.8	487	1	CPC5_RABIT	P00179 oryctolagus
264	6	1.8	421	1	GLTT_BACST	P24943 bacillus sc	337	6	1.8	487	1	CPCC_RABIT	P15123 oryctolagus
265	6	1.8	421	1	GLYA_HAEIN	P43844 haemophilus	338	6	1.8	489	1	CPCC_RABIT	P15123 oryctolagus
266	6	1.8	423	1	YCDB_ECOLI	P31345 escherichia	339	6	1.8	490	1	BAGR_LYMST	P36837 escherichia
267	6	1.8	426	1	AGAB_ECOLI	P42903 escherichia	340	6	1.8	490	1	CPCC_RAT	Q09323 lymnaea sta
268	6	1.8	426	1	CODA_ECOLI	P25524 escherichia	341	6	1.8	490	1	CPCC_RAT	P05178 rattus norv
269	6	1.8	426	1	GLAI_MYCTU	O53441 mycobacteri	342	6	1.8	490	1	CPCC_RAT	P11510 rattus norv
270	6	1.8	426	1	GLYA_MYCLE	O9x794 mycobacteri	343	6	1.8	490	1	CPCC_RAT	P20814 rattus norv
271	6	1.8	427	1	GLYA_STNY3	P77362 synchocyst	344	6	1.8	490	1	CPCC_MESAU	Q08078 mesocricetu
272	6	1.8	427	1	GLYA_THEMA	O9w219 thermotoga	345	6	1.8	490	1	CPCC_MESAU	P33263 mesocricetu
273	6	1.8	427	1	KDPA_HAEIN	P44806 haemophilus	346	6	1.8	490	1	CPCC_MOUSE	Q64458 mus musculu
274	6	1.8	428	1	DGRP_MYCSM	O52199 mycobacteri	347	6	1.8	490	1	CP23_MOUSE	P56655 mus musculu
275	6	1.8	428	1	FXB2_MOUSE	O64733 mus musculu	348	6	1.8	490	1	CP24_MOUSE	P56657 mus musculu
276	6	1.8	428	1	GLYA_AQUAE	O67776 aquifex aeo	349	6	1.8	491	1	CP2C_MOUSE	P56657 mus musculu
277	6	1.8	434	1	GLYA_HYEME	P34885 hypomicrob	350	6	1.8	491	1	YO6_CABEL	P34629 caenorhabd
278	6	1.8	437	1	SECT_STRCO	P46785 streptomyc	351	6	1.8	499	1	AINX_HUMAN	Q16332 homo sapien
279	6	1.8	437	1	SECT_STRGB	O59912 streptomyc	352	6	1.8	500	1	G6PD_SCHPO	Q00091 schizosacch
280	6	1.8	437	1	SECT_STRGR	O59916 streptomyc	353	6	1.8	501	1	TLCC_RICPR	Q92677 rickettsia
281	6	1.8	437	1	SECT_STRLI	P49977 streptomyc	354	6	1.8	502	1	ACHN_HUMAN	P17787 homo sapien
282	6	1.8	437	1	SECT_STRSC	P43416 streptomyc	355	6	1.8	502	1	DNA_MYCLE	P46388 mycobacteri
283	6	1.8	438	1	PAS5_RHOFA	P46377 rhodococcus	356	6	1.8	504	1	AINX_MOUSE	P46680 mus musculu
284	6	1.8	439	1	COMP_BOVIN	P35445 bos laurus	357	6	1.8	505	1	AINX_RAT	P23565 rattus norv
285	6	1.8	440	1	SCAL_DROME	P30052 drosophila	358	6	1.8	508	1	CP2B_HUMAN	Q15528 homo sapien
286	6	1.8	440	1	YA33_SCHPO	O09710 schizosacch	359	6	1.8	508	1	DNA_MYCAV	P49990 mycobacteri
287	6	1.8	443	1	HXA3_HUMAN	O43365 homo sapien	360	6	1.8	509	1	FTS2_CAVCR	P52972 caulobacter
288	6	1.8	445	1	ALCP_BACP3	P30145 bacillus ps	361	6	1.8	509	1	DNA_MYCPA	Q91717 mycobacteri
289	6	1.8	446	1	YX71_MYCTU	O50400 mycobacteri	362	6	1.8	509	1	STR_HYDAT	P17713 hydra atten
290	6	1.8	448	1	VIME_CRIGR	P48670 cricetus	363	6	1.8	511	1	DHAX_HUMAN	P49419 homo sapien
291	6	1.8	449	1	Y753_SYNY3	P74635 synchocyst	364	6	1.8	513	1	SYS_MERTH	Q27194 methanobact
292	6	1.8	451	1	PH71_PSEPU	Q05181 pseudomonas	365	6	1.8	514	1	YL06_CABEL	P46562 caenorhabd
293	6	1.8	451	1	UXAC_THEMA	O9wrx9 thermotoga	366	6	1.8	515	1	YL14_HUMAN	Q14154 homo sapien
294	6	1.8	453	1	PLST_CARAU	P31393 carassius a	367	6	1.8	520	1	TRPE_ECOLI	P00895 escherichia
295	6	1.8	454	1	NFM_PIG	P08552 sus scrofa	368	6	1.8	523	1	RNPF_RHOCA	O52718 rhodobacter
296	6	1.8	455	1	OPSD_OCTDO	P09241 octopus dof	369	6	1.8	524	1	G6PI_CHLMU	Q9PR16 chlamydia m
297	6	1.8	455	1	VIME_CYPCA	O92115 cyprinus ca	370	6	1.8	525	1	G6PI_CHLTR	Q84319 chlamydia t
298	6	1.8	456	1	PERI_XENLA	P48676 xenopus lae	371	6	1.8	526	1	4F2_MOUSE	P10832 mus musculu
299	6	1.8	457	1	DLDH_MYCGE	P47513 mycoplasma	372	6	1.8	526	1	G6PI_CHLPN	Q92674 chlamydia p
300	6	1.8	457	1	KLFS_HUMAN	O13887 homo sapien	373	6	1.8	529	1	TCPB_CABEL	P47207 caenorhabd
301	6	1.8	457	1	PLSB_PEA	P30706 pismus saliv	374	6	1.8	532	1	DCPS_BACHD	Q91997 bacillus ha
302	6	1.8	458	1	DESK_XENLA	P23229 xenopus lae	375	6	1.8	532	1	YKPS_CABEL	P34266 caenorhabd
303	6	1.8	458	1	MURA_CHLPN	Q9z7Y2 chlamydia p	376	6	1.8	543	1	P2CG_BOVIN	P79126 bos laurus
304	6	1.8	459	1	VIM1_XENLA	P24789 xenopus lae	377	6	1.8	544	1	SYK_MERTH	Q27585 methanobact
305	6	1.8	459	1	VIME_CHICK	P09654 gallus gall	378	6	1.8	545	1	VNCS_JCDNV	Q90054 junonia coe
306	6	1.8	461	1	VIME_ONCMY	P48674 oncorhynch	379	6	1.8	551	1	ETVA_HUMAN	P96605 thioobact
307	6	1.8	463	1	DESK_CHICK	P02542 gallus gall	380	6	1.8	552	1	YCGX_BACSU	Q91997 bacillus ha
308	6	1.8	463	1	VIM4_XENLA	P24790 xenopus lae	381	6	1.8	554	1	HYES_MOUSE	P34914 mus musculu
309	6	1.8	464	1	NU44_PARLI	P12775 paracentrot	382	6	1.8	555	1	ETVA_MOUSE	P28332 mus musculu
310	6	1.8	464	1	VIME_MESAU	P02544 mesocricetu	383	6	1.8	555	1	EPRB_MYCLE	Q33064 mycobacteri
311	6	1.8	465	1	YCF1_MARPO	P12223 marchantia	384	6	1.8	556	1	PRIS_THIFE	P96605 thioobact
312	6	1.8	465	1	VIME_BOVIN	P48616 bos laurus	385	6	1.8	557	1	G6PI_RABIT	Q91997 oryctolagus
313	6	1.8	465	1	VIME_HUMAN	P08670 homo sapien	386	6	1.8	558	1	Y322_MYCGE	P47564 mycoplasma
314	6	1.8	465	1	VIME_MOUSE	P20152 mus musculu	387	6	1.8	563	1	DEAD_MYCTU	Q11039 mycobacteri
315	6	1.8	465	1	VIME_RAT	P31000 rattus norv	388	6	1.8	565	1	Y322_MYCPN	P75323 mycoplasma
316	6	1.8	466	1	COO6_SCHPO	Q9y729 schizosacch	389	6	1.8	569	1	YAP3_YEAST	P32329 saccharomyc
317	6	1.8	466	1	G3BP_HUMAN	O13283 homo sapien	390	6	1.8	571	1	UGA4_YEAST	P32873 saccharomyc
318	6	1.8	468	1	DESM_MESAU	P02541 mesocricetu	391	6	1.8	574	1	LAMC_MOUSE	P11516 mus musculu
319	6	1.8	468	1	DESK_MOUSE	P31001 mus musculu	392	6	1.8	576	1	PABE_YEAST	P04147 saccharomyc
320	6	1.8	468	1	DESK_RAT	P48675 rattus norv	393	6	1.8	577	1	ORC2_HUMAN	Q13416 homo sapien
321	6	1.8	469	1	DESK_BOVIN	O62654 bos laurus	394	6	1.8	581	1	HEM1_STRCO	Q9w415 streptomyc
322	6	1.8	469	1	DESK_HUMAN	P17661 homo sapien	395	6	1.8	582	1	SYN2_HUMAN	Q92777 homo sapien
323	6	1.8	470	1	DESK_PIG	P02540 sus scrofa	396	6	1.8	583	1	LAM1_XENLA	P09010 xenopus lae
324	6	1.8	470	1	XNIF_XENLA	P35617 xenopus lae	397	6	1.8	586	1	SYN2_RAT	Q63337 rattus norv
325	6	1.8	473	1	ARSB_RAT	P50430 rattus norv	398	6	1.8	590	1	FTZ1_RHIME	P30327 rhizobium m

399	6	1.8	590	1	YKTA_CAEEL	P34327	caenorhabdi	472	6	1.8	811	1	MUTS_THEAQ	Q56215	thermus agu
400	6	1.8	591	1	Y875_CHTRR	084883	chlamydia t	473	6	1.8	817	1	MUTS_THECA	Q9216	thermus agu
401	6	1.8	598	1	FLIF_PSEAE	Q51463	pseudomonas	474	6	1.8	818	1	MUTS_THETH	Q56239	thermus agu
402	6	1.8	601	1	DEAD_BUCAI	P57453	buchnera ap	475	6	1.8	830	1	PKN2_MYXXA	P54736	myxococcus
403	6	1.8	601	1	HR78_DROME	Q24142	drosophila	476	6	1.8	831	1	NPH_RAT	P16884	rattus norv
404	6	1.8	608	1	GLMS_ECOLI	P17169	p glucosami	477	6	1.8	837	1	LDLR_RABIT	P20063	oryctolagus
405	6	1.8	609	1	GLMS_PASMU	P57963	p glucosami	478	6	1.8	845	1	NFM_MOUSE	P12839	rattus norv
406	6	1.8	610	1	CDPI_ARATH	O06880	arabidopsis	479	6	1.8	848	1	NFM_MOUSE	P08553	rattus norv
407	6	1.8	612	1	Y525_PSEAE	Q51464	pseudomonas	480	6	1.8	849	1	PRO5_YEAST	P121372	saccharomyc
408	6	1.8	613	1	DEAD_HAEIN	P45566	haemophilus	481	6	1.8	853	1	MUG2_RHIME	P56914	rhizobium m
409	6	1.8	615	1	SPPA_HAEIN	P45243	haemophilus	482	6	1.8	857	1	NFM_CHICK	P16035	gallus gall
410	6	1.8	623	1	DNAC_CAMJE	O69298	campylobact	483	6	1.8	859	1	DD24_HUMAN	Q99277	homo sapien
411	6	1.8	626	1	HTPG_BACSU	P46208	bacillus su	484	6	1.8	859	1	YD48_MYCTU	Q11018	homo sapien
412	6	1.8	628	1	DEAD_ECOLI	P23304	escherichia	485	6	1.8	859	1	DSC2_HUMAN	Q02487	homo sapien
413	6	1.8	628	1	SYL_NOSLO	Q27707	nosma locu	486	6	1.8	901	1	PIP_IACIA	P49022	lactococcus
414	6	1.8	636	1	GYRB_THEMA	P77993	thermotoga	487	6	1.8	902	1	PEPB_XENIA	Q91736	xenopus lae
415	6	1.8	637	1	YHM1_YEAST	P38856	saccharomyc	488	6	1.8	904	1	SECA_RHOCA	P52966	rhodobacter
416	6	1.8	639	1	LACY_LEUIA	Q48624	leuconostoc	489	6	1.8	907	1	NUOG_ECOLI	P33602	escherichia
417	6	1.8	642	1	DEAD_KLEPN	P33906	klebsiella	490	6	1.8	907	1	NUOG_ECOLI	P33900	salmonella
418	6	1.8	642	1	DNAC_FRATU	P48205	francisella	491	6	1.8	910	1	PERT_BORPE	P14283	bordetella
419	6	1.8	643	1	GAG_SEV3L	P27400	similan foam	492	6	1.8	911	1	PERT_BORBR	P07197	homo sapien
420	6	1.8	643	1	YNVA_CAEEL	P34567	caenorhabdi	493	6	1.8	915	1	NFM_HUMAN	P24338	homo sapien
421	6	1.8	644	1	NFM_RABIT	P54938	oryctolagus	494	6	1.8	922	1	PERT_HUMAN	Q32483	rhodopseudo
422	6	1.8	646	1	NA95_HUMAN	O91u6	homo sapien	495	6	1.8	936	1	CAPP_RHOPA	P21851	homo sapien
423	6	1.8	647	1	VEI_HPVS2	P36730	human papil	496	6	1.8	937	1	A2B1_HUMAN	Q06078	saccharomyc
424	6	1.8	657	1	LAMA_CHICK	P13648	gallus gall	497	6	1.8	939	1	YL09_YEAST	O50968	neisseria g
425	6	1.8	664	1	LAMA_HUMAN	P02545	homo sapien	498	6	1.8	950	1	UVRA_NEIGO	Q06441	xenopus lae
426	6	1.8	665	1	LAMA_MOUSE	P48678	mus musculu	499	6	1.8	955	1	TSP4_XENIA	P32618	saccharomyc
427	6	1.8	665	1	LAMA_MOUSE	P48679	rattus norv	500	6	1.8	956	1	YEP3_YEAST	P32618	saccharomyc
428	6	1.8	665	1	LAMA_XENIA	P11048	mycoplasma	501	6	1.8	961	1	TSP4_HUMAN	P35443	homo sapien
429	6	1.8	665	1	HMW3_MYCPN	O50360	mycoplasma	502	6	1.8	968	1	BCAL_RAT	Q63767	rattus norv
430	6	1.8	672	1	HMW3_MYCPN	P53070	saccharomyc	503	6	1.8	969	1	DPOM_NEUTN	P33538	neurospora
431	6	1.8	679	1	MT01_YEAST	O13582	homo sapien	504	6	1.8	971	1	Y029_HUMAN	O15032	homo sapien
432	6	1.8	683	1	BGH3_HUMAN	O07837	homo sapien	505	6	1.8	979	1	PTPN_MOUSE	O60673	mus musculu
433	6	1.8	685	1	SC31_HUMAN	P30001	human herpe	506	6	1.8	980	1	TSP4_MOUSE	P49774	rattus norv
434	6	1.8	694	1	VGLH_HSV6U	P52543	human herpe	507	6	1.8	983	1	YL14_HUMAN	O14157	homo sapien
435	6	1.8	694	1	VGLH_HSV6U	O08893	manduca sex	508	6	1.8	984	1	EPB1_HUMAN	Q07494	gallus gall
436	6	1.8	699	1	E75_MANSE	P06660	trypanosoma	509	6	1.8	984	1	EPB1_CHICK	P54762	homo sapien
437	6	1.8	705	1	ADDC_RAT	O62847	rattus norv	510	6	1.8	984	1	EPB1_HUMAN	P09759	rattus norv
438	6	1.8	705	1	MLMD_STRCO	O9x4b6	streptomyce	511	6	1.8	986	1	DPO1_SYNY3	O55971	synchocyst
439	6	1.8	706	1	ADDC_MOUSE	O9qyb5	mus musculu	512	6	1.8	986	1	DPO1_SYNY3	O62889	rattus norv
440	6	1.8	707	1	NU5C_MALAR	O9mvy2	malayiviscus	513	6	1.8	1018	1	DPOC_SCHPO	O12704	schizosacch
441	6	1.8	709	1	NU5C_PACAO	O9mvy2	pachira agu	514	6	1.8	1018	1	HIRA_CHICK	P79967	gallus gall
442	6	1.8	711	1	E75_GALME	P50239	galleria me	515	6	1.8	1020	1	NFH_HUMAN	P12036	homo sapien
443	6	1.8	714	1	PILO_PSEAE	P34750	pseudomonas	516	6	1.8	1027	1	ISWI_DROME	Q24368	drosophila
444	6	1.8	716	1	IKKE_HUMAN	O14164	homo sapien	517	6	1.8	1030	1	SPAB_BACSU	P39774	bacillus su
445	6	1.8	717	1	IKKE_MOUSE	O9ic08	mus musculu	518	6	1.8	1039	1	Y410_RHISN	P55517	rhizobium s
446	6	1.8	717	1	NAH4_MOUSE	P26434	rattus norv	519	6	1.8	1043	1	CHS2_PABBR	O92444	paracoccidi
447	6	1.8	717	1	NAH4_MOUSE	P09130	escherichia	520	6	1.8	1064	1	SYL_AERPE	O9y167	aeropyrum p
448	6	1.8	718	1	YSO2_CAEEL	O10128	caenorhabdi	521	6	1.8	1069	1	RNT1_CAEEL	O76512	caenorhabdi
449	6	1.8	722	1	HMW2_DROME	P22808	drosophila	522	6	1.8	1084	1	HDW4_HUMAN	P56524	homo sapien
450	6	1.8	723	1	HR96_DROME	Q24143	drosophila	523	6	1.8	1087	1	NFH_MOUSE	P19246	mus musculu
451	6	1.8	732	1	PSAA_HETTR	O9xgv3	heterocapsa	524	6	1.8	1092	1	LIFR_MOUSE	P42703	mus musculu
452	6	1.8	744	1	RELA_ECOLI	P11585	escherichia	525	6	1.8	1096	1	KPC1_ASFNG	O00078	aspergillus
453	6	1.8	753	1	METE_SALTY	O916n1	salmonella	526	6	1.8	1114	1	TCF8_CHICK	P36197	gallus gall
454	6	1.8	755	1	COMP_RAT	P35444	rattus norv	527	6	1.8	1118	1	UBP8_HUMAN	P10221	herpes simp
455	6	1.8	757	1	COMP_HUMAN	P49747	homo sapien	528	6	1.8	1123	1	V120_HSV11	O14687	homo sapien
456	6	1.8	761	1	NETR_MOUSE	O08762	mus musculu	529	6	1.8	1157	1	Y182_HUMAN	P19246	mus musculu
457	6	1.8	765	1	AOC3_MOUSE	O70423	mus musculu	530	6	1.8	1173	1	DPOL_RCMVM	O85428	rat cytoleg
458	6	1.8	766	1	SAK1_SCHPO	P48383	schizosacch	531	6	1.8	1211	1	DP3A_HELPJ	O921f9	helicobacte
459	6	1.8	769	1	ITB2_BOVIN	P32592	bos taurus	532	6	1.8	1211	1	DP3A_HELPJ	P56157	helicobacte
460	6	1.8	769	1	ITB2_BOVIN	P53114	sus scrofa	533	6	1.8	1225	1	VGL2_CVPRM	P27455	porcine res
461	6	1.8	770	1	A4_MOUSE	P12023	mus musculu	534	6	1.8	1225	1	VGL2_CVPRM	P24413	porcine res
462	6	1.8	770	1	A4_MOUSE	P08592	rattus norv	535	6	1.8	1231	1	BLM_CAEEL	O18017	caenorhabdi
463	6	1.8	774	1	RRP3_INCBE	P21770	influenza c	536	6	1.8	1247	1	POLS_ONVNG	P22056	o'nyong-nyo
464	6	1.8	774	1	RRP3_INCBE	P21770	influenza c	537	6	1.8	1256	1	ATL_STRAU	P52081	staphylococ
465	6	1.8	778	1	FTSK_INCBU	P39920	coxiella bu	538	6	1.8	1257	1	PER2_MOUSE	O54943	mus musculu
466	6	1.8	781	1	GCS1_CAEEL	Q19426	caenorhabdi	539	6	1.8	1262	1	CA13_CHICK	P12105	gallus gall
467	6	1.8	785	1	YHY2_YEAST	P38870	saccharomyc	540	6	1.8	1270	1	VGLN_CHICK	P81021	gallus gall
468	6	1.8	798	1	UNR_HUMAN	O75534	homo sapien	541	6	1.8	1297	1	PUR4_VIBCH	O9K92	vibrio chol
469	6	1.8	798	1	UNR_RAT	P18395	rattus norv	542	6	1.8	1302	1	UBPY_CAEEL	O09931	caenorhabdi
470	6	1.8	802	1	ACSB_ACEXY	P37716	acetobacter	543	6	1.8	1317	1	YAOF_SCHPO	O10094	schizosacch
471	6	1.8	810	1	NFM_BOVIN	O77788	bos taurus	544	6	1.8	1329	1	FTSK_ECOLI	P46889	escherichia

545	6	1.8	1331	1	CTA2_HUMAN	Q9uhc6	homo sapien	618	5	1.5	55	1	V6K_BDVP	P09518	barley yell
546	6	1.8	1332	1	XKDO_BACSU	P54334	baecillus su	619	5	1.5	57	1	A4_PIG	Q09023	sus scrofa
547	6	1.8	1335	1	XDH_DROME	P10351	drosophila	620	5	1.5	57	1	A4_URSWA	Q09149	ursus marit
548	6	1.8	1365	1	STZ2_DROME	P25172	drosophila	621	5	1.5	58	1	A4_CANFA	Q28280	cantis famli
549	6	1.8	1381	1	CTAL_RAT	P97846	rattus norv	622	5	1.5	58	1	A4_RABIT	Q28748	oryctolagus
550	6	1.8	1384	1	CTAL_HUMAN	P78357	homo sapien	623	5	1.5	58	1	A4_SHEEP	Q28757	ovis aries
551	6	1.8	1385	1	CTAL_MOUSE	Q54391	mus musculu	624	5	1.5	59	1	A4_BOVIN	Q28053	bos taurus
552	6	1.8	1425	1	MADI_HUMAN	Q54305	homo sapien	625	5	1.5	60	1	RLJ2_DEIRA	P49328	delinococcus
553	6	1.8	1440	1	SYEP_HUMAN	P07814	homo sapien	626	5	1.5	61	1	RS21_SYNY3	P48931	synchocyst
554	6	1.8	1441	1	VGLM_BUNL7	P09612	bunyavirus	627	5	1.5	60	1	YVDH_VACCV	P48316	vaccinia vl
555	6	1.8	1447	1	VGL2_CVPRU	Q02167	porcine tra	628	5	1.5	62	1	COXS_MOUSE	P56394	mus musculu
556	6	1.8	1447	1	VGL2_CVPRU	P07946	porcine tra	629	5	1.5	62	1	STAF_HUMAN	P28608	homo sapien
557	6	1.8	1447	1	VGL2_CVPRU	Q01977	porcine tra	630	5	1.5	62	1	YZ05_MERTU	Q60262	methanococ
558	6	1.8	1449	1	VGL2_CVPRU	P18450	porcine tra	631	5	1.5	64	1	BCNR_CLOPE	P15366	clostridium
559	6	1.8	1449	1	VGL2_CVPRU	P33470	porcine tra	632	5	1.5	66	1	YSCB_YEREN	Q01246	yersinia en
560	6	1.8	1451	1	VGL2_CVCAT	P36300	canine ente	633	5	1.5	68	1	NLR2_PUAR	P82353	prunus arme
561	6	1.8	1452	1	VGL2_FIPV	P10033	feline infe	634	5	1.5	68	1	S61G_CAEEL	Q19697	caenorhabd
562	6	1.8	1461	1	TOR2_CANAL	P87078	candida alb	635	5	1.5	68	1	YRP3_AZOCA	P33988	azochitobiu
563	6	1.8	1476	1	APSA_EMENT	Q00083	emeritocella	636	5	1.5	71	1	CER1_CERCA	P36190	ceratilis c
564	6	1.8	1687	1	CCAM_MUSDO	Q25452	musca domes	637	5	1.5	71	1	CER2_CERCA	O17512	ceratilis c
565	6	1.8	1691	1	YLH4_CAEEL	P34358	caenorhabd	638	5	1.5	74	1	MCPB_BOVIN	P80343	bos taurus
566	6	1.8	1701	1	U520_HUMAN	Q75643	homo sapien	639	5	1.5	74	1	YCA7_OIOSI	P49542	odontella s
567	6	1.8	1744	1	TENS_CHICK	Q04205	gallus gall	640	5	1.5	75	1	PSK_ASPOF	Q9f510	asparagus o
568	6	1.8	1745	1	ZOI_MOUSE	P39447	mus musculu	641	5	1.5	75	1	S100_LEPPA	P82378	lepidosiren
569	6	1.8	1772	1	MSP1_PLAYO	P13828	plasmodium	642	5	1.5	77	1	PSKS_ARATH	Q91264	arabidopsis
570	6	1.8	1794	1	YAV1_SCHPO	Q10172	schizosacch	643	5	1.5	77	1	RUXG_YEAST	P23822	saccharomye
571	6	1.8	1816	1	APF6_HUMAN	P55196	homo sapien	644	5	1.5	77	1	YAML_STRYL	P23822	saccharomye
572	6	1.8	1862	1	ANK1_MOUSE	Q02357	mus musculu	645	5	1.5	78	1	Y055_TREPA	Q83094	treponema p
573	6	1.8	2326	1	POLG_HPAV2	P26580	hepatitis a	646	5	1.5	78	1	Y150_TREPA	Q98924	ureaplasma
574	6	1.8	2326	1	POLG_HPAV4	P26581	hepatitis a	647	5	1.5	78	1	YRPX_ECOLI	P52134	escherichia
575	6	1.8	2326	1	POLG_HPAV8	P26582	hepatitis a	648	5	1.5	79	1	DEP1_STOCA	O16136	stomoxys ca
576	6	1.8	2327	1	POLG_HPAV8	P08617	hepatitis a	649	5	1.5	79	1	NUSN_LEMCA	Q34879	lemur catla
577	6	1.8	2327	1	POLG_HPAV1	P08617	hepatitis a	650	5	1.5	79	1	YE09_STRCO	Q69880	streptomyce
578	6	1.8	2327	1	POLG_HPAV4	P13301	hepatitis a	651	5	1.5	80	1	AFPI_BRANA	P30225	brassica na
579	6	1.8	2330	1	POLG_HPAV5	P14553	simlan hepa	652	5	1.5	81	1	Y00H_BPT4	P39418	bacteriocal
580	6	1.8	2333	1	POLG_EMADV	P03305	f genome po	653	5	1.5	81	1	Y334_ARCFU	Q29913	archaeoglob
581	6	1.8	2397	1	MOKR_SCHPO	Q09854	schizosacch	654	5	1.5	81	1	YMAJ_ECOLI	P76036	escherichia
582	6	1.8	2469	1	TEGU_HSVSA	Q01056	hepsevitus	655	5	1.5	81	1	Y002_BPL2	P42337	bacterioph
583	6	1.8	2482	1	VWF_PIG	Q28833	sus scrofa	656	5	1.5	82	1	HFO_PSEAE	Q9hnm0	pseudomonas
584	6	1.8	2515	1	TUD_DROME	P25823	drosophila	657	5	1.5	82	1	MLC1_DROME	Q24399	drosophila
585	6	1.8	2516	1	CCAD_DROME	Q24270	drosophila	658	5	1.5	82	1	MLC1_DROSE	Q24656	drosophila
586	6	1.8	3149	1	TEGU_EBV	P03186	epstein-bar	659	5	1.5	82	1	MLC1_DROTE	Q24656	drosophila
587	6	1.8	3411	1	POLG_YEYV1	P03314	y genome po	660	5	1.5	83	1	HPIS_THIRO	Q24766	drosophila
588	6	1.8	3411	1	POLG_YEYV2	P13901	y genome po	661	5	1.5	83	1	HPIS_THETI	P80176	thermochrom
589	6	1.8	3415	1	POLG_POWVL	Q04338	t genome po	662	5	1.5	83	1	V67_BPT3	P20330	bacterioph
590	6	1.8	3418	1	BRC2_HUMAN	P51587	homo sapien	663	5	1.5	85	1	BM02_HUMAN	Q9af12	homo sapien
591	6	1.8	3672	1	LM12_CAEEL	Q21313	caenorhabd	664	5	1.5	85	1	BM02_MOUSE	Q09352	mus musculu
592	6	1.8	3695	1	LMAS_HUMAN	Q15330	homo sapien	665	5	1.5	85	1	HPIS_THIRO	P00261	thiocapsa r
593	6	1.8	3726	1	ABF1_MOUSE	Q61329	mus musculu	666	5	1.5	86	1	Y12K_MSVS	P14593	maize stre
594	6	1.8	3828	1	TRX_DROVI	Q24742	drosophila	667	5	1.5	86	1	OAG1_VTBCH	Q9ahk2	vidrio chol
595	6	1.8	4543	1	LRP1_CHICK	P98157	gallus gall	668	5	1.5	86	1	R31B_STRPY	Q9a016	streptococc
596	5	1.5	11	1	ULAG_HUMAN	P31333	homo sapien	669	5	1.5	86	1	REV_HV123	P05667	human immu
597	5	1.5	15	1	PDGB_PIG	P20034	sus scrofa	670	5	1.5	86	1	RS17_BACHD	Q92835	baecillus ha
598	5	1.5	18	1	SPAF_HELAN	P81098	heliannthus	671	5	1.5	86	1	RS17_BACSU	P11284	baecillus su
599	5	1.5	21	1	TKNC_CARAU	P25421	carassius a	672	5	1.5	86	1	RS17_STRPN	Q94403	streptococc
600	5	1.5	34	1	COL_CHICK	P11148	gallus gall	673	5	1.5	86	1	VE7_HPV10	P36618	human papil
601	5	1.5	37	1	PMP1_RAT	P18889	rattus norv	674	5	1.5	87	1	RS20_ZYMO	Q92500	zymomonas m
602	5	1.5	40	1	PMP1_YEAST	P32093	saccharomye	675	5	1.5	87	1	VE7_HPV28	P50783	human papil
603	5	1.5	43	1	COAT_BPPHL	Q07485	bacterioph	676	5	1.5	88	1	ATPE_CHILL	P35111	chlocaapsa
604	5	1.5	43	1	PSBF_SYNY3	P09191	synchocyst	677	5	1.5	88	1	COXK_BOVIN	P13183	bos taurus
605	5	1.5	45	1	TRXB_VIBF1	P80892	vibrio fisci	678	5	1.5	88	1	C070_LOCOM	P80232	locusta mig
606	5	1.5	46	1	LMH1_RHOPA	P03156	bos taurus	679	5	1.5	88	1	EF1B_THEAC	Q95hnl	thermoplasm
607	5	1.5	48	1	POPI_BOVIN	P35107	rhodopsedu	680	5	1.5	88	1	Y4BB_RHISN	P55369	rhizobium s
608	5	1.5	50	1	INS_PLAFE	P09477	platichtlys	681	5	1.5	88	1	FLIO_RHISN	P55597	rhizobium s
609	5	1.5	51	1	GIP_CANFA	P02727	canis famli	682	5	1.5	89	1	IM9A_HUMAN	P35535	baecillus su
610	5	1.5	52	1	NU3K_NEUCR	Q35141	neutrospora	683	5	1.5	89	1	IM9A_MOUSE	Q94517	homo sapien
611	5	1.5	52	1	RUBR_DESVH	P00269	desulfovibr	684	5	1.5	89	1	SLTB_BP933	Q94518	mus musculu
612	5	1.5	52	1	RUBR_DESVH	P15412	desulfovibr	685	5	1.5	89	1	XHLA_BACSU	P09386	bacterioph
613	5	1.5	53	1	LHA1_RHOAC	P35089	rhodopsedu	686	5	1.5	89	1	YCO2_PARDE	P39798	baecillus su
614	5	1.5	53	1	LHA2_RHOAC	P35090	rhodopsedu	687	5	1.5	90	1	PTSO_PROMI	P08302	paracoccus
615	5	1.5	55	1	ATP8_PELISU	Q79674	pelomedusa	688	5	1.5	90	1	VE7_HPV29	Q92864	proteus mir
616	5	1.5	55	1	PER_CLOST	P80168	clostridium	689	5	1.5	92	1	IM13_DROME	P50784	human papil
617	5	1.5	55	1	PER_CLOST	P80168	clostridium	690	5	1.5	92	1	IM13_DROME	Q9vnc3	drosophila

691	5	1.5	92	1	SP12_ARATH	Q944j0 arabidopsis	764	5	1.5	108	1	PRVB_CYPCA	P02618 cyprinus ca
692	5	1.5	92	1	YC23_METJA	Q58620 methanococ	765	5	1.5	108	1	Y826_RICR	Q94201 rickettsia
693	5	1.5	92	1	YPS1_SYNP2	P31525 synechococc	766	5	1.5	108	1	YC54_PORR	P51204 porphyra pu
694	5	1.5	92	1	VR13_CORAM	Q45825 corynebacte	767	5	1.5	108	1	YD31_MYCE	P53423 mycobacteti
695	5	1.5	93	1	NODE_RHIME	P06232 rhizobium m	768	5	1.5	109	1	HMG_C_HUMAN	P52926 mycobacteti
696	5	1.5	93	1	U185_ARATH	Q9CA23 arabidopsis	769	5	1.5	109	1	NIOM_HUMAN	P56181 homo sapien
697	5	1.5	93	1	Y01C_CAEEL	Q09283 caenorhabdi	770	5	1.5	109	1	PRVA_TRISE	P30563 tritakis sem
698	5	1.5	94	1	YBJH_ECOLI	P75808 escherichia	771	5	1.5	109	1	R31B_CHLN	Q92669 chlamydia p
699	5	1.5	94	1	Y0Y3_CAEEL	P34661 caenorhabdi	772	5	1.5	109	1	YIRI_YEAS	P40404 saccharomyc
700	5	1.5	95	1	DBH_THETH	P14366 thernus aqu	773	5	1.5	109	1	YX_BACSH	P39044 bacillus sp
701	5	1.5	95	1	I13A_HUMAN	Q9uh18 homo sapien	774	5	1.5	110	1	CYOD_PSEPU	Q9wrt4 pseudomonas
702	5	1.5	95	1	I13B_HUMAN	Q9y514 homo sapien	775	5	1.5	110	1	HMGB_CHITE	P40623 chironomus
703	5	1.5	95	1	R37A_HALNI	Q9hs98 halobacteri	776	5	1.5	110	1	PEPA_BOVIN	P00792 bos taurus
704	5	1.5	95	1	RL23_BACST	P04454 bacillus st	777	5	1.5	110	1	RLA4_SCHPO	P17478 schizosacch
705	5	1.5	95	1	RR20_CYPAP	P48140 cyanophora	778	5	1.5	111	1	FLIE_BORR	P52609 borrelia bu
706	5	1.5	95	1	YVBC_VACCC	P20543 vaccinia vi	779	5	1.5	111	1	PHNA_ECOLI	P16680 escherichia
707	5	1.5	95	1	YI1_ORYSA	Q23810 oryza sativ	780	5	1.5	111	1	RLAI_CAEEL	P91913 caenorhabdi
708	5	1.5	96	1	CATC_ACICA	Q43932 acinetobact	781	5	1.5	111	1	VE7_HPVO7	P36816 human papil
709	5	1.5	96	1	RT24_SCHPO	Q43020 schizosacch	782	5	1.5	112	1	CORT_RAT	Q62949 rattus norv
710	5	1.5	96	1	U185_CHLRE	Q94ey2 chlamydomon	783	5	1.5	112	1	GLNB_AQUAE	Q65513 aquilex aeo
711	5	1.5	96	1	VE7_HPVO6	Q80942 human papil	784	5	1.5	112	1	HMGD_DROME	Q05783 drosophilla
712	5	1.5	97	1	DEFA_HUMAN	P12838 homo sapien	785	5	1.5	112	1	YBAV_HAEIN	Q57134 haemophilus
713	5	1.5	97	1	HFO_NEIMA	Q9jqw6 neisseria m	786	5	1.5	112	1	YFIA_ECOLI	P11285 escherichia
714	5	1.5	97	1	NO73_MEDSA	P11728 medicago sa	787	5	1.5	113	1	H3B_STYRE	P81202 stylyonchia
715	5	1.5	98	1	CYTB_HUMAN	P04080 homo sapien	788	5	1.5	113	1	HIBF_KLEPN	Q91004 klebsiella
716	5	1.5	98	1	Z126_HUMAN	P35275 homo sapien	789	5	1.5	113	1	HYBF_MORMO	Q9zhn1 moronegella
717	5	1.5	99	1	IHFA_PASHA	P55166 pasteurella	790	5	1.5	113	1	LCCL1_LEUGE	P34035 leucostoc
718	5	1.5	99	1	MCPA_BOVIN	P28201 bos taurus	791	5	1.5	113	1	REV_HVIJ3	P12484 human immun
719	5	1.5	99	1	SY02_HUMAN	P13500 homo sapien	792	5	1.5	113	1	YCVI_MYCTU	Q11048 mycobacteri
720	5	1.5	99	1	SY02_MACFA	Q9myu4 macaca fasc	793	5	1.5	114	1	YELG_ECOLI	P33917 escherichia
721	5	1.5	99	1	SY02_PIG	P42831 sus scrofa	794	5	1.5	114	1	Y211_METJA	P62921 methanococc
722	5	1.5	99	1	SY08_HUMAN	P80075 homo sapien	795	5	1.5	114	1	MOO_KLEPN	Q32719 klebsiella
723	5	1.5	100	1	BPT2_BOVIN	P04815 bos taurus	796	5	1.5	115	1	REV_HVIMN	P05871 human immun
724	5	1.5	100	1	R181_PINTH	P52763 pinus thunb	797	5	1.5	115	1	RLA2_HUMAN	Q29387 homo sapien
725	5	1.5	100	1	V07K_NMY	P15068 narctissus m	798	5	1.5	115	1	RLA2_PIG	Q29387 homo sapien
726	5	1.5	100	1	Y151_ARCFU	Q30066 archaeoglob	799	5	1.5	115	1	Y4HO_RHISN	P02401 rattus norv
727	5	1.5	100	1	Y908_HAEIN	P44073 haemophilus	800	5	1.5	115	1	YIDR_ECOLI	P50339 escherichia
728	5	1.5	100	1	YC83_ARCFU	Q28985 archaeoglob	801	5	1.5	115	1	YXEA_BACSH	P54945 escherichia
729	5	1.5	101	1	CH10_HUMAN	Q04984 homo sapien	802	5	1.5	115	1	NU3M_CHICK	P54945 escherichia
730	5	1.5	101	1	CH10_MOUSE	Q64433 mus musculu	803	5	1.5	116	1	NU3M_LARCK	P18998 gallus gall
731	5	1.5	101	1	CH10_MOUSE	P26772 rattus norv	804	5	1.5	116	1	YXIS_APP22	Q03371 latimeria c
732	5	1.5	101	1	SY02_CANFA	P52203 canis fami1	805	5	1.5	116	1	REV_HVIJR	P20689 human immun
733	5	1.5	101	1	THP_HUMAN	P20962 homo sapien	806	5	1.5	116	1	GSPI_VIBCH	P04889 bacteriopho
734	5	1.5	101	1	Y941_HAEIN	P44082 haemophilus	807	5	1.5	117	1	NU3M_PLASU	P45775 vibrio chol
735	5	1.5	101	1	ATPN_BOVIN	Q10642 mycobacteri	808	5	1.5	117	1	NU3M_PLASU	Q34950 lumbricus t
736	5	1.5	102	1	U185_ORYSA	Q28652 bos taurus	809	5	1.5	117	1	VATG_MANSE	Q36518 platyomas
737	5	1.5	102	1	Y198_MSVN	P14574 maize strea	810	5	1.5	117	1	REV_HVIEL	P55880 rhizobium s
738	5	1.5	102	1	Y198_MSVN	Q07734 mycobacteri	811	5	1.5	117	1	THH3_ARATH	Q39421 human immun
739	5	1.5	102	1	Y198_MSVN	P14574 maize strea	812	5	1.5	117	1	TRH4_ECOLI	Q00190 escherichia
740	5	1.5	102	1	Y198_MSVN	Q07734 mycobacteri	813	5	1.5	118	1	Y493_HAEIN	Q05023 haemophilus
741	5	1.5	103	1	Y198_MSVN	P14574 maize strea	814	5	1.5	118	1	Y914_AQUAE	Q67059 aquilex aeo
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743	5	1.5	104	1	Y198_MSVN	P14574 maize strea	816	5	1.5	118	1	YHAI_ECOLI	P42622 escherichia
744	5	1.5	104	1	Y198_MSVN	P14574 maize strea	817	5	1.5	118	1	YHAI_ECOLI	Q09399 caenorhabdi
745	5	1.5	104	1	Y198_MSVN	P14574 maize strea	818	5	1.5	118	1	YHAI_ECOLI	P16242 caenorhabdi
746	5	1.5	104	1	Y198_MSVN	P14574 maize strea	819	5	1.5	118	1	YHAI_ECOLI	Q77530 callitriche
747	5	1.5	104	1	Y198_MSVN	P14574 maize strea	820	5	1.5	118	1	YHAI_ECOLI	P01816 homo sapien
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749	5	1.5	104	1	Y198_MSVN	P14574 maize strea	822	5	1.5	118	1	YHAI_ECOLI	P41133 mus musculu
750	5	1.5	105	1	Y198_MSVN	P14574 maize strea	823	5	1.5	119	1	YHAI_ECOLI	P41138 rattus norv
751	5	1.5	106	1	Y198_MSVN	P14574 maize strea	824	5	1.5	119	1	YHAI_ECOLI	Q62953 rattus norv
752	5	1.5	106	1	Y198_MSVN	P14574 maize strea	825	5	1.5	119	1	YHAI_ECOLI	P41711 antherea p
753	5	1.5	106	1	Y198_MSVN	P14574 maize strea	826	5	1.5	119	1	YHAI_ECOLI	Q39362 brassica na
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838	5	1.5	121	1	FLIT_ECOLI	P26610 escherichia	911	5	1.5	134	1	CYS1_ARATH	Q42342 rhodospirillum rubrum
839	5	1.5	121	1	PA22_CERGO	P81165 cerophididlo	912	5	1.5	134	1	GYRB_RHOCA	P23860 arbidopsis
840	5	1.5	121	1	RNPA_NEIMB	Q91366 neisseria m	913	5	1.5	135	1	FENR_SHIFL	P29801 shigella fl
841	5	1.5	121	1	YC84_METUA	O58680 methanococc	914	5	1.5	135	1	LEG2_CONMY	O99102 conger myr1
842	5	1.5	121	1	YCF2_VICFA	P15821 vicia faba	915	5	1.5	135	1	VAL2_ICMV	O08589 indian cass
843	5	1.5	122	1	HP15_CHRVI	P01260 chromacium	916	5	1.5	135	1	VE6_PAPVD	P03128 deer papill
844	5	1.5	122	1	HV3G_HOMAN	P01768 homo sapien	917	5	1.5	136	1	MCH_MERTO	O99103 methyllococ
845	5	1.5	122	1	INL3_MOUSE	O09107 mus musculu	918	5	1.5	136	1	NRD1_ECOLI	Q47415 escherichia
846	5	1.5	122	1	MP13_LYMST	P80090 lymphaea sta	919	5	1.5	136	1	NRD1_SALTY	O56109 salmonella
847	5	1.5	123	1	RCRB_PYRHO	O59171 pyrococcus	920	5	1.5	136	1	RK16_MESVI	O9muk3 mesostigma
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851	5	1.5	124	1	RIBT_BACSU	P17622 bacillus su	924	5	1.5	137	1	NU3M_PODAN	P15680 podospora a
852	5	1.5	124	1	SPOE_BACSU	P06628 bacillus su	925	5	1.5	137	1	RK16_ODOSI	P04953 odontella s
853	5	1.5	124	1	VARE_NEUCR	O99756 neosporea	926	5	1.5	137	1	YSCB_YEREN	O01243 yeroinia en
854	5	1.5	124	1	YB28_YEAST	P38296 saccharomyc	927	5	1.5	138	1	ARPU_STRTK	O34055 streptococc
855	5	1.5	124	1	YC69_MYCTU	Q11050 mycobacteri	928	5	1.5	138	1	NLJ3_PARKU	Q40005 parietaria
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857	5	1.5	125	1	GLHA_FUNHE	P47744 fundulus su	930	5	1.5	139	1	RL16_TREPA	O83326 treponema p
858	5	1.5	125	1	PFDB_HALNI	O94580 halobacteri	931	5	1.5	139	1	RS16_SPROCO	O99879 streptomyc
859	5	1.5	125	1	PVP_CHRSA	P81046 chromolaus	932	5	1.5	139	1	Y589_HAEIN	O86668 streptomyc
860	5	1.5	125	1	SV02_PABIT	P28292 cryetolaus	933	5	1.5	139	1	Y589_HAEIN	P44020 haemophilus
861	5	1.5	125	1	SYB_LOIPE	P47194 loligo peal	934	5	1.5	140	1	ADPX_ARATH	O91881 arabidopsis
862	5	1.5	126	1	C10_MOUSE	O35127 mus musculu	935	5	1.5	140	1	PAAI_ECOLI	P76591 saccharomyc
863	5	1.5	126	1	HV2A_HOMAN	P01814 homo sapien	936	5	1.5	140	1	POPT_YEAST	P38291 saccharomyc
864	5	1.5	126	1	YVAB_BACSU	P37516 bacillus su	937	5	1.5	140	1	RIN4_BPPHA	Q03182 bacterioph
865	5	1.5	127	1	CYCP_ALCXX	P00138 alcaligenes	938	5	1.5	140	1	RS12_CAEEL	P49196 caenorhabd1
866	5	1.5	127	1	NIR1_METTH	O26703 methanobact	939	5	1.5	140	1	VE6_HPV1A	P06629 human papil
867	5	1.5	127	1	RT08_ACACA	P46757 acanthamoeb	940	5	1.5	140	1	VMFG_LAMBD	P03734 bacterioph
868	5	1.5	127	1	SPG1_DICDI	P15519 dictyostell	941	5	1.5	140	1	YDAT_ECOLI	P76604 escherichia
869	5	1.5	127	1	SPG2_DICDI	P15521 dictyostell	942	5	1.5	141	1	HBAD_GEONI	P83124 geochelone
870	5	1.5	127	1	SPG3_DICDI	P15521 dictyostell	943	5	1.5	141	1	HBAD_PHACA	P10781 phalacrocor
871	5	1.5	128	1	YAKH_RHISM	P55228 rhizobium s	944	5	1.5	141	1	HBAD_PHRIM	P02062 phytophys hl
872	5	1.5	128	1	CUEB_HAEIN	P46517 haemophilus	945	5	1.5	141	1	HBAD_SPHPU	P10062 sphendonop p
873	5	1.5	128	1	LSHB_STRCA	P80664 struthio ca	946	5	1.5	141	1	HBA_CAMDR	P01974 camelus dro
874	5	1.5	128	1	RBEA_HAEIN	P45141 haemophilus	947	5	1.5	141	1	HBA_LAMGL	P01973 lama glama
875	5	1.5	128	1	RS9_THETH	P80374 thermus aqu	948	5	1.5	141	1	HBA_LAMPA	P07426 lama guanica
876	5	1.5	128	1	Y070_TREPA	O83109 treponema p	949	5	1.5	141	1	HBA_VICUN	P07425 lama vicuna
877	5	1.5	129	1	DYLA_CHLRE	O39591 chlamydomon	950	5	1.5	141	1	HBB_DASAK	P56692 dasayella ak
878	5	1.5	129	1	IHPA_WYXXA	O94617 myxococcus	951	5	1.5	141	1	NPEI_RHIME	O52393 rhizobium m
879	5	1.5	129	1	VAL2_ABMVW	P21944 abutellon mo	952	5	1.5	141	1	VE6_HPV38	O80907 human papil
880	5	1.5	129	1	VAL2_TCMV	P03562 tomatlo gold	953	5	1.5	141	1	YEBB_VTBPA	P40610 vldrio para
881	5	1.5	129	1	VAL2_TMOV	O06658 tomatlo mot	954	5	1.5	142	1	A2S1_HUMAN	P53680 homo sapien
882	5	1.5	129	1	VH07_VACCV	P08586 vaccinia vi	955	5	1.5	142	1	A2S1_MOUSE	O00808 mus musculu
883	5	1.5	129	1	Y207_AERPE	O99162 aeropyrum p	956	5	1.5	142	1	NCR1_YEAST	P40096 saccharomyc
884	5	1.5	129	1	YABR_ECOLI	P52096 escherichia	957	5	1.5	142	1	VC46_BPM15	O05557 mycobacteri
885	5	1.5	130	1	ACPS_MYCLE	O94763 mycobacteri	958	5	1.5	143	1	PFID2_DROME	O9965 drosophila
886	5	1.5	130	1	ACPS_MYCTU	O53328 mycobacteri	959	5	1.5	143	1	RISB_ARCFU	O28152 archaeglob
887	5	1.5	130	1	OREX_CANFA	O99166 canis famli	960	5	1.5	143	1	RS12_YEAST	P48589 saccharomyc
888	5	1.5	130	1	RS9_CLOAB	O99163 clostridium	961	5	1.5	143	1	YIIB_ECOLI	P37688 escherichia
889	5	1.5	130	1	RS9_STRPV	O99008 streptococc	962	5	1.5	144	1	G20U_BACSU	P80879 bacillus su
890	5	1.5	130	1	Y497_RICPR	O92450 rickettsia	963	5	1.5	144	1	GLB3_LAMSP	P15466 lamelliabrac
891	5	1.5	130	1	YERH_YEREN	P31490 yeroinia en	964	5	1.5	144	1	HEX8_ADE12	P03284 human adeno
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894	5	1.5	131	1	OREX_PIG	O77668 sus scrofa	967	5	1.5	145	1	YIGO_YEAST	P18019 saccharomyc
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896	5	1.5	131	1	RS6E_HALNI	O9hmj5 halobacteri	969	5	1.5	145	1	HBBA_CAPHI	P02077 capra hircu
897	5	1.5	131	1	RS6E_METUA	P54067 methanococc	970	5	1.5	145	1	HBFB_BOVIN	P02081 bos taurus
898	5	1.5	131	1	VAL2_SLICV	P27445 squash leaf	971	5	1.5	145	1	HBAB_ALCAA	P02073 bos taurus
899	5	1.5	131	1	Y293_AQUAE	O66643 aquifex aeo	972	5	1.5	145	1	HBAB_BISBO	P09422 alces alces
900	5	1.5	132	1	MCH_METAL	O99164 methylomict	973	5	1.5	145	1	HBAB_BOSGF	P02071 bos gaurus
901	5	1.5	132	1	MCU_METRU	O99162 methylomona	974	5	1.5	145	1	HBAB_BOSMU	P02072 bos mutus g
902	5	1.5	132	1	RS19_PASMU	P57872 pasteurella	975	5	1.5	145	1	HBAB_BOVIN	P02070 bos taurus
903	5	1.5	132	1	RS19_PYRAB	O99169 pyrococcus	976	5	1.5	145	1	HBAB_OVINU	P02076 ovis orient
904	5	1.5	132	1	RS19_PYRHO	O59422 pyrococcus	977	5	1.5	145	1	HBAB_TRAST	P04245 tregelaphus
905	5	1.5	132	1	VG14_BPBO3	O37895 bacterioph	978	5	1.5	145	1	PAZ0_BUNMU	P01531 locusta mig
906	5	1.5	132	1	VG25_BPT4	P09425 bacterioph	979	5	1.5	145	1	PSAN_HORUV	P00606 bungarus mu
907	5	1.5	133	1	ATPE_CVACA	O9tm40 cyanidium c	980	5	1.5	145	1	RL11_AQUAE	P31093 hordeum vul
908	5	1.5	133	1	NL21_PARJU	P55958 parietaria	981	5	1.5	145	1	YAP4_SCHPO	O67758 aquifex aeo
909	5	1.5	133	1	POB8_YEAST	P38208 saccharomyc	982	5	1.5	145	1		O09658 schizosacch

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983 5 1.5 145 1 YERC_SCHPO 014095 schizosacch
984 5 1.5 145 1 YTKA_BACSU P40768 bacillus su
985 5 1.5 146 1 CYM5_RAP P04166 ratus norv
986 5 1.5 146 1 HBB1_CYMA P23017 cygnodrac
987 5 1.5 146 1 HBB1_MOUSE P02088 mus musculu
988 5 1.5 146 1 HBB1_PAGBO P03348 pagochenta
989 5 1.5 146 1 HBB2_MOUSE P02089 mus musculu
990 5 1.5 146 1 HBB2_PANLE P18968 panthera le
991 5 1.5 146 1 HBB2_TRENE O93349 trematomus
992 5 1.5 146 1 HBB_AEGMO P07418 aegyplus mo
993 5 1.5 146 1 HBB_AILFU P18982 alfurus ful
994 5 1.5 146 1 HBB_AILME P18983 alfurus ful
995 5 1.5 146 1 HBB_ANAPL P02114 anas platyr
996 5 1.5 146 1 HBB_ANAPP P02115 anas platyr
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1000 5 1.5 146 1 HBB_AOTTR P02035 actus trivi

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ALIGNMENTS

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RESULT 1
ZIPA_ECOLI STANDARD: PRT: 328 AA.
AC P77773;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cell division protein zipa.
GN ZIPA OR B2412.
OS Escherichia coli.
OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-PB103;
RX MEDLINE-97160838; PubMed-9008158;
RA Hale C.A., de Boer P.A.J.;
RT "Direct binding of FtsZ to Zipa, an essential component of the septal
RL ring structure that mediates cell division in E. coli.";
RN Cell 88:175-185(1997).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE-97426617; PubMed-9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE-97349980; PubMed-9205837;
RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Oshima T., Oyama S., Saito N., Sempel G., Satoh Y., Sivasubram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
RT -K12 genome corresponding to 50.0-68.8 min on the linkage map and
RL analysis of its sequence features.";
RN DNA Res. 4:91-113(1997).
[4]
RP STRUCTURE BY NMR OF 185-328.
RX MEDLINE-20384201; PubMed-10924108;
RA Moy F.J., Glasfeld E., Mosyak L., Powers R.;
RT "Solution structure of zipa, a crucial component of Escherichia coli

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RT cell division.";
RL Biochemistry 39:9146-9156(2000).
CC -1- FUNCTION: Interacts directly with the cell division protein ftsz.
CC Probable receptor for the septal ring structure, may anchor it
CC to the inner-membrane.
CC -1- SUBCELLULAR LOCATION: Type IB membrane protein. Inner membrane.
CC -1- SIMILARITY: BELONGS TO THE ZIPA FAMILY.
CC -----
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CC -----
DR EMBL: U74650; AABA2061.1; -.
DR EMBL: AE000329; AAC75465.1; -.
DR EMBL: D90870; BAA16284.1; -.
DR PDB: 1F7X; 28-JUN-01.
DR PDB: 1F7W; 28-JUN-01.
DR ECGene: EGI4169; zipa.
KW Cell division; Septation; Transmembrane; Inner membrane; 3D-structure;
KW Complete proteome.
FT DOMAIN 1 6 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 7 27 POTENTIAL.
FT DOMAIN 28 328 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 211 211 A -> L (IN REF. 2).
SQ SQUENCE 328 AA: 36433 MW: 020F1197153F9BAD CRC64;

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Query Match 100.0%; Score 328; DB 1; Length 328;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 328; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MMODRLITLITVGAIALVHGFTSKRERSMFRDRPLKMKSKRDDSDYDEVEDD 60
DB 1 MMODRLITLITVGAIALVHGFTSKRERSMFRDRPLKMKSKRDDSDYDEVEDD 60
QY 61 EGVGEVVRHVRNHPANAQHEAARSPQHQQPPYASAPROPVQOQPPAQQVPPQHAPH 120
DB 61 EGVGEVVRHVRNHPANAQHEAARSPQHQQPPYASAPROPVQOQPPAQQVPPQHAPH 120
QY 121 PAQPVQOQPAYQPOPEQPLQOQVSPQVAPAPQVHSAAPQPAQQAQFQPAEPVAPQPEVAP 180
DB 121 PAQPVQOQPAYQPOPEQPLQOQVSPQVAPAPQVHSAAPQPAQQAQFQPAEPVAPQPEVAP 180
QY 181 PAPVMDKPKRKEAVITIMNVAHHGSELNGBALNLSIQAGFTIGDMNITVHRHLSPPGSGP 240
DB 181 PAPVMDKPKRKEAVITIMNVAHHGSELNGBALNLSIQAGFTIGDMNITVHRHLSPPGSGP 240
QY 241 ALFSLANWVKPGTFDEEMKDFTPGVITFMQVPSYSGDELQNFKLMLQSAQHIADVEGVV 300
DB 241 ALFSLANWVKPGTFDEEMKDFTPGVITFMQVPSYSGDELQNFKLMLQSAQHIADVEGVV 300
QY 301 LDDQRRMMPQKLEKYODIIREVKDANA 328
DB 301 LDDQRRMMPQKLEKYODIIREVKDANA 328
RESULT 2
ZIPA_SALTY STANDARD: PRT: 328 AA.
AC P55894;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DE 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cell division protein zipa.
GN ZIPA OR STM2428 OR STM2664.
OS Salmonella typhimurium, and
OS Salmonella typhi.
OC Bacteria: Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.

```

OX NCBI_TaxID=602, 601;
 [1]
 RN SEQUENCE FROM N.A.
 RP SPECIES-S. typhimurium; STRAIN-LT2 / SSC1412 / ATCC 700720;
 RC MEDLINE-21334948; PubMed-11677609;
 RA McLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porcollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of *Salmonella enterica* serovar Typhimurium
 LT2.";
 RL Nature 413:852-856(2001).
 RN [2]
 RP SEQUENCE OF 1-32 FROM N.A.
 RC SPECIES-S. typhimurium; STRAIN-LT2;
 RX MEDLINE-88257033; PubMed-3290198;
 RA Byrne C.R., Monroe R.S., Ward K.A., Kredich N.M.;
 RT "DNA sequences of the *cysK* regions of *Salmonella typhimurium* and
 RT *Escherichia coli* and linkage of the *cysK* regions to *ptsH*.";
 RL J. Bacteriol. 170:3150-3157(1988).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES-S. typhimurium; STRAIN-CT18;
 RX MEDLINE-21534947; PubMed-11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrett B.G.;
 RT "Complete genome sequence of a multiple drug resistant *Salmonella*
 RT *enterica* serovar Typhimurium CT18.";
 RL Nature 413:848-853(2001).
 CC -1- FUNCTION: Interacts directly with the cell division protein *ftsZ*.
 CC Probable receptor for the septal ring structure, may anchor it
 CC to the inner-membrane (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type IB membrane protein. Inner membrane (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE ZIPA FAMILY.
 CC -----
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 CC -----
 CC EMBL: AE008809; AL21322.1; -;
 DR EMBL: M21450; -; NOT ANNOTATED-CDS.
 DR EMBL: AL627274; CND07660.1; -;
 KW StyGene; SGI0748; zipA.
 KW Cell division; Septation; Transmembrane; Inner membrane;
 KW Complete proteome.
 KW DOMAIN 1 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 7 27 POTENTIAL.
 FT DOMAIN 28 328 CYTOPLASMIC (POTENTIAL).
 FT SEQUENCE 328 AA: 36318 MW: 88444708 kDa; BBA44F708AFA35F13 CRC64;
 SO
 Query Match 16.5%; Score 54; DB 1; Length 328;
 Best Local Similarity 100.0%; Pred. No. 3; 5e-47;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MMODELIIIVGAIIVIALVHGFWTSRRKSSMFRDPLKMKSKRDDSD 54
 DB 1 MMODELIIIVGAIIVIALVHGFWTSRRKSSMFRDPLKMKSKRDDSD 54
 RESULT 3

ZIPA_YERPE
 ID ZIPA_YERPE STANDARD; PRT; 328 AA.
 AC P58492;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Cell division protein zipA homolog.
 GN ZIPA OR YPO2990.
 OS *Yersinia pestis*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Yersinia*.
 OX NCBI_TaxID=632;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CO-92 / Biovar Orientalis;
 RX MEDLINE-21470413; PubMed-11586360;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Felwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
 RT "Genome sequence of *Yersinia pestis*, the causative agent of plague.";
 RL Nature 413:523-527(2001).
 CC -1- FUNCTION: Interacts directly with the cell division protein *ftsZ*.
 CC Probable receptor for the septal ring structure, may anchor it
 CC to the inner-membrane (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type IB membrane protein. Inner membrane (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE ZIPA FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AJ141454; CAC92234.1; -;
 KW Cell division; Septation; Transmembrane; Inner membrane;
 KW Complete proteome.
 KW DOMAIN 1 PERIPLASMIC (POTENTIAL).
 FT TRANSMEM 5 25 POTENTIAL.
 FT DOMAIN 26 328 CYTOPLASMIC (POTENTIAL).
 FT SEQUENCE 328 AA: 36098 MW: 80489084 kDa; EA04B89084649044 CRC64;
 SO
 Query Match 3.4%; Score 11; DB 1; Length 328;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 242 LFSLANVWPKG 252
 DB 239 LFSLANVWPKG 249
 RESULT 4
 ID MBR1_YEAST STANDARD; PRT; 339 AA.
 AC P23493;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE MBR1 protein.
 GN MBR1 OR YKL093W OR YKL440.
 OS *Saccharomyces cerevisiae* (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC *Saccharomycetales*; *Saccharomycetaceae*; *Saccharomyces*.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-R100;
 RX MEDLINE-94268503; PubMed-8208248;
 RA Dalgman-Fornier B., Nguyen C.C., Reisdorf P., Lemeignan B.,
 RA Bolotin-Fukuhara M.;
 RT "MBR1 and MBR3, two related yeast genes that can suppress the growth
 RT defect of hap2, hap3 and hap4 mutants.";
 RL Mol. Genet. 243:575-583(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RX MEDLINE-94078677; PubMed-8256524;
 RA Paller C., Valens M., Puzos V., Fukuhara H., Cheret G., Sor F.,
 RA Bolotin-Fukuhara M.;
 RT "DNA sequence analysis of a 17 kb fragment of yeast chromosome XI
 RT physically localizes the MBR1 gene and reveals eight new open reading
 RT frames, including a homologue of the KIN1/KIN2 and SNF1 protein
 RT kinases.";
 RL Yeast 9:1149-1155(1993).
 RN [3]
 RP SEQUENCE OF 169-339 FROM N.A.
 RX MEDLINE-94262329; PubMed-8203166;
 RA James C.M., Gent M.E., Oliver S.G.;
 RT "Sequence analysis of a 3.5 Kb EcoRI fragment from the left arm of
 RT Saccharomyces cerevisiae chromosome XI reveals the location of the
 RT MBR1 gene and a sequence related to a GTPase-activating protein.";
 RL Yeast 10:257-264(1994).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE-92215853; PubMed-1725263;
 RA Valens M., Rinaidi T., Dalgman-Fornier B., Bolotin-Fukuhara M.;
 RT "Identification of nuclear genes which participate to mitochondrial
 RT translation in Saccharomyces cerevisiae.";
 RL Biochimie 73:1525-1532(1991).
 CC -1- FUNCTION: PARTICIPATES IN MITOCHONDRIAL BIOGENESIS.
 CC -1- SIMILARITY: STRONG, TO MBR3.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M63309; AAA88725.1; -
 DR EMBL: X71133; CA50464.1; -
 DR EMBL: X75561; CA53240.1; -
 DR EMBL: Z28093; CA81931.1; -
 DR PIR: S37920; S37920.
 DR SGD: S0001576; MBR1.
 KW Mitochondrion.
 FT CONFLICT 88 A -> G (IN REF. 1).
 FT CONFLICT 168 G -> R (IN REF. 1).
 FT CONFLICT 206 S -> T (IN REF. 1).
 FT CONFLICT 245 G -> E (IN REF. 1).
 SQ SEQUENCE 339 AA; 36934 MW; A38E7EA7049754A0 CRC64;

Query Match 2.4%; Score 8; DB 1; Length 339;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 100 OPROPOQO 107
 DB 305 OPROPOQO 312
 RESULT 5
 ID YHNS_ECOLI STANDARD; PRT: 419 AA.
 AC P37621;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein yhns.
 GN YHNS OR B3473.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 ON NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R12 / MG1655;
 RX MEDLINE-94316500; PubMed-8041620;
 RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
 RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
 RT region from 76.0 to 81.5 minutes.";
 RL Nucleic Acids Res. 22:2576-2586(1994).
 CC -----
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 CC -----
 DR EMBL: U00039; CAB34656.1; -
 DR EMBL: AE000423; AAC76498.1; -
 DR EcoGene: Egi2219; yhns.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 419 AA; 43783 MW; 2260CA0E17438CFE CRC64;

Query Match 2.4%; Score 8; DB 1; Length 419;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 175 PEPVAPPA 182
 DB 16 PEPVAPPA 23
 RESULT 6
 ID BCHB_CHLNU STANDARD; PRT: 541 AA.
 AC 09F6X5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Light-independent protochlorophyllide reductase subunit B
 DE (EC 1.18.-.-) (Li-POR subunit B) (DPOR subunit B).
 GN BCHB.
 OS Chloroflexus aurantiacus.
 OC Bacteria; Green non-sulfur bacteria; Chloroflexaceae group;
 OC Chloroflexaceae; Chloroflexus.
 ON NCBI_TaxID=1108;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20433268; PubMed-10976061;
 RA Xiong J., Fischer W.M., Inoue K., Nakahara M., Bauer C.E.;
 RT "Molecular evidence for the early evolution of photosynthesis.";
 RL Science 289:1724-1730(2000).
 CC -----
 CC -1- FUNCTION: Uses Mg-ATP and reduced ferredoxin to reduce ring D of
 CC protochlorophyllide (Pchl) to form chlorophyllide a (Chlide)
 CC (By similarity). This reaction is light-independent.
 CC -1- PATHWAY: Light-independent bacteriochlorophyll biosynthesis.
 CC -1- SUBUNIT: Protochlorophyllide reductase is thought to be composed
 CC of three subunits: bchl, bchm and bchb. Could form a
 CC heterotrimer of two bchl and two bchm subunits.
 CC -1- SIMILARITY: BELONGS TO THE CHLB / BCHB / BCHZ FAMILY.
 CC -----
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CC -----
CC DR EMBL: AF288460: AAG15210.1: -
CC DR Interpro: IPR000510: Oxidored_nitrognse_1.
CC DR Pfam: PF00148: oxidored_nitro; 2.
CC DR Oxidoreductase; Photosynthesis; Bacteriochlorophyll biosynthesis.
CC KW SEQUENCE 541 AA: 59181 MW: 0F3060E48358A5F7 CRC64;
CC
CC Query Match 2.4%; Score 8; DB 1; Length 541;
CC Best Local Similarity 100.0%; Pred. No. 3.9;
CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Oy 177 PVAEPAPV 184
CC |||||
CC Db 445 PVAEPAPV 452
CC
CC
CC RESULT 7
CC ALU8_HUMAN STANDARD: PRT: 591 AA.
CC ID ALU8_HUMAN
CC AC P39195:
CC DT 01-FEB-1995 (Rel. 31, Created)
CC DT 01-FEB-1995 (Rel. 31, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Alu subfamily SX sequence contamination warning entry.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CC NCBI_TaxId=9606;
CC
CC [1]
CC RP SEQUENCE FROM N.A.
CC RA MEDLINE-95021758; PubMed-7935834;
CC RA Claverie J.-M.; Makalowski W.;
CC RT "Alu alert."
CC RT Nature 371:752-752(1994).
CC RL [2]
CC RP CONCEPT.
CC RP MEDLINE-92241891; PubMed-1572661;
CC RA Claverie J.-M.;
CC RT "Identifying coding exons by similarity search: alu-derived and other
CC RT potentially misleading protein sequences.";
CC RL Genomics 12:838-841(1992).
CC RN [3]
CC RP ALU FAMILIES CLASSIFICATION.
CC RP MEDLINE-88333009; PubMed-3138422;
CC RA Quentin Y.;
CC RT "The Alu family developed through successive waves of fixation
CC RT closely connected with primate lineage history.";
CC RL J. Mol. Evol. 27:194-202(1988).
CC RN [4]
CC RP ALU FAMILIES CLASSIFICATION.
CC RP MEDLINE-91178815; PubMed-1706781;
CC RA Jurka J.; Milosavljevic A.;
CC RT "Reconstruction and analysis of human Alu genes.";
CC RL J. Mol. Evol. 32:105-121(1991).
CC CC -1- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
CC THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CC CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
CC FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
CC REPEATS.
CC CC -1- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CC CODON, 'xxx' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC CC -1- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER
CC POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
CC ACID SEQUENCES.
CC CC -1- CAUTION: GENUINE SEQUENCES ARE INTERSPERSED IN HUMAN AND
CC PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE
CC ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN
CC ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER,
CC CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS

CC LIGATED WITH ALU-DERIVED SEQUENCE IN ANY ORIENTATION. ALTHOUGH ALU
CC ELEMENTS (ESPECIALLY SITUATED ON THE COMPLEMENTARY STRAND) HAVE A
CC GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS,
CC CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
CC OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
CC CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING
CC DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
CC THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
CC BEING REPORTED.
CC CC -1- CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE
CC WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A
CC PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
CC CODING NUCLEOTIDE SEQUENCE.
CC
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CC CC
CC DR EMBL: U14574; -; NOT_ANNOTATED_CDS.
CC KM Hypothetical protein
CC FT DOMAIN 1 96 FRAME-1.
CC FT DOMAIN 1 100 195 FRAME-2.
CC FT DOMAIN 199 294 FRAME-3.
CC FT DOMAIN 298 393 FRAME-4.
CC FT DOMAIN 397 492 FRAME-5.
CC FT DOMAIN 496 591 FRAME-6.
CC SQ SEQUENCE 591 AA: 64395 MW: AC8154AD8A6B280 CRC64;
CC
CC
CC Query Match 2.4%; Score 8; DB 1; Length 591;
CC Best Local Similarity 100.0%; Pred. No. 4.2;
CC Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC Oy 244 SLANWKP 251
CC |||||
CC Db 227 SLANWKP 234
CC
CC
CC RESULT 8
CC ALU7_HUMAN STANDARD: PRT: 593 AA.
CC ID ALU7_HUMAN
CC AC P39194;
CC DT 01-FEB-1995 (Rel. 31, Created)
CC DT 01-FEB-1995 (Rel. 31, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Alu subfamily SQ sequence contamination warning entry.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
CC NCBI_TaxId=9606;
CC
CC [1]
CC RP SEQUENCE FROM N.A.
CC RA MEDLINE-95021758; PubMed-7935834;
CC RA Claverie J.-M.; Makalowski W.;
CC RT "Alu alert."
CC RT Nature 371:752-752(1994).
CC RL [2]
CC RP CONCEPT.
CC RP MEDLINE-92241891; PubMed-1572661;
CC RA Claverie J.-M.;
CC RT "Identifying coding exons by similarity search: alu-derived and other
CC RT potentially misleading protein sequences.";
CC RL Genomics 12:838-841(1992).
CC RN [3]
CC RP ALU FAMILIES CLASSIFICATION.
CC RP MEDLINE-88333009; PubMed-3138422;
CC RA Quentin Y.;
CC RT "The Alu family developed through successive waves of fixation
CC RT closely connected with primate lineage history.";
CC RL J. Mol. Evol. 27:194-202(1988).
CC RN [4]
CC RP ALU FAMILIES CLASSIFICATION.
CC RP MEDLINE-91178815; PubMed-1706781;
CC RA Jurka J.; Milosavljevic A.;
CC RT "Reconstruction and analysis of human Alu genes.";
CC RL J. Mol. Evol. 32:105-121(1991).
CC CC -1- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF.3 AND REF.4) INDICATE
CC THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
CC CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
CC FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
CC REPEATS.
CC CC -1- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
CC CODON, 'xxx' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
CC CC -1- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER
CC POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
CC ACID SEQUENCES.
CC CC -1- CAUTION: GENUINE SEQUENCES ARE INTERSPERSED IN HUMAN AND
CC PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE
CC ACTIVELY TRANSCRIBED BY POL III. NORMAL TRANSCRIPTS MAY CONTAIN
CC ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER,
CC CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS

RL J. Mol. Evol. 27:194-202(1988).
 RN [4]
 RP ALU FAMILIES CLASSIFICATION.
 RX MEDLINE-91178815; PubMed-1706781;
 RA Jurka J., Milosavljevic A.;
 RT "Reconstruction and analysis of human Alu genes.";
 RL J. Mol. Evol. 32:105-121(1991).
 CC -1- MISCELLANEOUS: VARIOUS ANALYSES (SEE REF. 3 AND REF. 4) INDICATE
 CC THAT ALU REPEATS FALL INTO 8 SUBFAMILIES. THEREFORE, 8 ALU WARNING
 CC CONSENSUS SEQUENCES HAVE BEEN CONSTITUTED THAT CONTAIN ALL SIX
 CC FRAMES CONCEPTUAL TRANSLATIONS OF EACH OF THESE CLASSES OF ALU
 CC REPEATS.
 CC -1- MISCELLANEOUS: ISOLATED 'X' INDICATES THE PRESENCE OF A STOP
 CC CODON, 'XXX' IS USED TO SEPARATE THE VARIOUS TRANSLATION PHASES.
 CC -1- CAUTION: THIS ALU ENTRY IS PROVIDED IN ORDER TO AVOID THE FURTHER
 CC POLLUTION OF PROTEIN SEQUENCE DATABASES WITH ALU-DERIVED AMINO
 CC ACID SEQUENCES.
 CC -1- CAUTION: ALU REPETITIVE SEQUENCES ARE INTERSPERSED IN HUMAN AND
 CC PRIMATE GENOMES WITH AN AVERAGE SPACING OF 4 KB. SOME OF THEM ARE
 CC ACTIVELY TRANSCRIBED BY POL. III. NORMAL TRANSCRIPTS MAY CONTAIN
 CC ALU-DERIVED SEQUENCES IN 5' OR 3' UNTRANSLATED REGIONS. HOWEVER,
 CC CDNA LIBRARIES ALSO CONTAIN PARTIAL AND/OR REARRANGED CDNAS
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 CC GREAT POTENTIAL TO CREATE ADDITIONAL/ALTERNATIVE EXONS.
 CC CONSIDERATION SHOULD BE GIVEN TO THE POSSIBILITY THAT THE PRESENCE
 CC OF AN ALU IN AN OPEN READING FRAME MAY HAVE RESULTED FROM A
 CC CLONING ARTIFACT OR MAY BE DUE TO MISINTERPRETATION OF SEQUENCING
 CC DATA. THIS POINT HAS BEEN OVERLOOKED ON SEVERAL OCCASIONS, WITH
 CC THE CONSEQUENCE OF ERRONEOUS ALU-DERIVED AMINO ACID SEQUENCES
 CC BEING REPORTED.
 CC -1- CAUTION: ANY SIGNIFICANT SIMILARITY OF A PUTATIVE PROTEIN SEQUENCE
 CC WITH AN ALU-TRANSLATED ENTRY MUST BE TAKEN AS A WARNING THAT A
 CC PART OF ALU REPEAT MAY HAVE BEEN ARTIFACTUALLY INCLUDED IN THE
 CC CODING NUCLEOTIDE SEQUENCE.
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 CC -----
 CC EMBL: U14573; -; NOT_ANNOTATED_CDS.
 DR KW Hypothetical protein.
 FT DOMAIN 1 97
 FT DOMAIN 101 196 FRAME-1.
 FT DOMAIN 200 295 FRAME-2.
 FT DOMAIN 299 395 FRAME-3.
 FT DOMAIN 399 494 FRAME-4.
 FT DOMAIN 498 593 FRAME-5.
 FT DOMAIN 593 644 FRAME-6.
 SQ SEQUENCE 593 AA; 64417 MW; 54A4F50F33A6089F CRC64;
 Query Match 2.4%; Score 8; DB 1; Length 593;
 Best Local Similarity 100.0%; Pred. No. 4.2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 244 SLANWKP 251
 Db 228 SLANWKP 235
 RESULT 9
 LHA3_ECTHA STANDARD; PRT; 49 AA.
 AC P80107;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Light-harvesting protein B800/850/890, alpha-3 chain (EHA-alpha-3)
 DE (Antenna pigment protein, alpha-3 chain) (Fragment).

OS Ectochlorodospira halophila.
 OC Bacteria; Proteobacteria; gamma subdivision; Ectochlorodospiraceae;
 OC Halorhodospira.
 OX NCBI_TaxID=1053;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=DSM 244;
 RX MEDLINE=92249336; PubMed=1577009;
 RA Wagner-Huber R., Brunsholz R.A., Bissig I., Frank G., Suter F.,
 RA Zuber H.;
 RT "The primary structure of the antenna polypeptides of
 RT Ectochlorodospira halochloris and Ectochlorodospira halophila. Four
 RT core-type antenna polypeptides in E. halochloris and E. halophila.";
 RL Eur. J. Biochem. 205:917-925(1992).
 CC -1- FUNCTION: ANTENNA COMPLEXES ARE LIGHT-HARVESTING SYSTEMS, WHICH
 CC TRANSFER THE CORE COMPLEX ENERGY TO THE REACTION CENTERS.
 CC -1- SUBUNIT: THE CORE COMPLEX IS FORMED BY DIFFERENT ALPHA AND BETA
 CC CHAINS. BINDING BACTERIOCHLOROPHYLL MOLECULES, AND ARRANGED
 CC MOST PROBABLY IN TETRAMERIC STRUCTURES DISPOSED AROUND THE
 CC REACTION CENTER. THE NON-PIGMENTED GAMMA CHAINS MAY CONSTITUTE
 CC ADDITIONAL COMPONENTS.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Inner membrane.
 CC PIR: S23290; S23290.
 DR HSP: P26789; 1K2U.
 DR InterPro: IPR002361; Antenna_comp_alpha.
 DR InterPro: IPR000066; LHC.
 DR Pfam: PF00556; LHC; 1.
 DR PROSITE: PS00968; ANTENNA_COMP_ALPHA; 1.
 KW Antenna complex; Light-harvesting polypeptide; Transmembrane;
 KW Magnesium; Bacteriochlorophyll; Inner membrane.
 FT DOMAIN 1 14 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 15 35 POTENTIAL.
 FT DOMAIN 36 >49 PERIPLASMIC (POTENTIAL).
 FT METAL 31 31 AXIAL LIGAND TO THE BACTERIOCHLOROPHYLL
 FT FT MAGNESIUM (POTENTIAL).
 SQ NON_TER 49 49
 SQ SEQUENCE 49 AA; 5479 MW; 753BFC2EC2014419 CRC64;
 Query Match 2.1%; Score 7; DB 1; Length 49;
 Best Local Similarity 100.0%; Pred. No. 4.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 18 IALLVHG 24
 Db 26 IALLVHG 32
 RESULT 10
 RL17_LEPIN STANDARD; PRT; 178 AA.
 AC Q9XD08;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 50S ribosomal protein L17.
 GN RPLQ.
 OS Leptospira interrogans.
 OC Bacteria; Spirochaetales; Leptospiraceae; Leptospira.
 OX NCBI_TaxID=173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SEROVAR LAI;
 RX MEDLINE=20088835; PubMed=10620683;
 RA Zuercher R.L., Hartskeerl R.A., van de Kemp H., Bal A.E.;
 RT "Characterization of the Leptospira interrogans S10-spc-alpha
 RT operon.";
 RL FEMS Microbiol. Lett. 182:303-308(2000).
 CC -1- SIMILARITY: BELONGS TO THE L17P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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CC -----
DR EMBL: AF115283: AAD40611.1: -
DR InterPro: IPR000456: Ribosomal_L17.
DR Pfam: PF01196: Ribosomal_L17: 1.
DR ProDom: PD004277: Ribosomal_L17: 1.
DR PROSITE: PS01167: RIBOSOMAL_L17: 1.
KW Ribosomal protein.
SQ SEQUENCE 178 AA: 20902 MW: FB06DCE4950B5740 CRC64:

Query Match 2.1%; Score 7; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 TSKERS 33
DB 125 TSKERS 131

RESULT 11
RS3A_HALN1 STANDARD; PRT; 206 AA.
ID RS3A_HALN1
AC Q9HRA5;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30S ribosomal protein S3Ae.
GN RPS3AE OR RPS3E OR VMG0787G.
OC Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxId=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Shroana J.,
RA Swartzell S., Welt D., Hall J., Dahl T.A., Welt R., Goo Y.A.,
RA Leitzhauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Madocks D.G., Jadhavski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Beck R.F., Pohnschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
CC -1- SIMILARITY: BELONGS TO THE S3AE FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL: AE005021: AAC19253.1: -
DR InterPro: IPR001593: Ribosomal_S3AE.
DR Pfam: PF01015: Ribosomal_S3AE: 1.
DR ProDom: PD003035: Ribosomal_S3AE: 1.
DR PROSITE: PS01191: RIBOSOMAL_S3AE: FALSE_NEG.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 206 AA: 23362 MW: 8E5033F7AA28D60 CRC64:

Query Match 2.1%; Score 7; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 210 EALLNSI 216

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DB 151 EALLNSI 157

RESULT 12
GRPS_MYXXA STANDARD; PRT; 255 AA.
ID GRPS_MYXXA
AC P95333;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Grps protein.
GN GRPS.
OC Myxococcus xanthus.
OC Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
OC Myxococcales; Cytophacteriineae; Myxococcaceae; Myxococcus.
OX NCBI_TaxId=34;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=DK1622;
RA Weimer R., Hartzell P.L., Youderian P.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: POTENTIAL CHAPERONE FOR OTHER PROTEINS INVOLVED IN
CC SOCIAL MORTILITY.
CC -1- SIMILARITY: BELONGS TO THE GRPE FAMILY.
CC -----
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CC -----
DR EMBL: U83800: AAC64204.1: -
DR HSSP: P09372: IDKG.
DR InterPro: IPR000740: GRPE.
DR Pfam: PF01025: GRPE: 1.
DR PRINTS: PR00773: GRPEPROTEIN.
DR PROSITE: PS01071: GRPE: 1.
KW Chaperone.
SQ SEQUENCE 255 AA: 27390 MW: 7A41F433563D10C0 CRC64:

Query Match 2.1%; Score 7; DB 1; Length 255;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 166 PAEPVAA 172
DB 216 PAEPVAA 222

RESULT 13
TRT1_HUMAN STANDARD; PRT; 277 AA.
ID TRT1_HUMAN
AC P13805;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tropoin T, slow skeletal muscle isoforms (Slow skeletal muscle
DE tropoin T).
GN TNNI1 OR TNN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88058976; PubMed=2824479;
RA Gahlmann R., Trout A.B., Wade R.P., Gunning P., Kedes L.;
RT "Alternative splicing generates variants in important functional
RT domains of human slow skeletal tropoin T."

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RN J. Biol. Chem. 262:16122-16126(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Skeletal muscle.
RX MEDLINE=9418326; PubMed=8135831;
RA Samsen F., Mesnard L., Mihovilovic M., Potter T.G., Mercadier J.-J.,
RA Roses A.D., Gilbert J.R.;
RT "A new human slow skeletal troponin T (TnTs) mRNA isoform derived
RT from alternative splicing of a single gene."
RL Biochem. Biophys. Res. Commun. 199:841-847(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=9920866; PubMed=10191089;
RA Barton P.J.R., Cullen M.E., Townsend P.J., Brand N.J., Mullen A.J.,
RA Norman D.A.M., Bhavsar P.K., Yacoub M.H.;
RT "Close physical linkage of human troponin genes: organization,
RT sequence, and expression of the locus encoding cardiac troponin I and
RT slow skeletal troponin T."
RL Genomics 57:102-109(1999).
CC -1- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF
CC TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERES
CC CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HERE), 2 AND 3; ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
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CC -----
DR EMBL: M19309; AAA61204.1; -
DR EMBL: M19308; AAA61205.1; -
DR EMBL: S69208; AAB30272.1; -
DR EMBL: S69209; AAB30273.1; -
DR EMBL: A7011712; CAA09751.1; -
DR EMBL: A7011713; CAA09752.1; JOINED.
DR EMBL: A7011712; CAA09752.1; -
DR EMBL: A7011713; CAA09752.1; JOINED.
DR PIR: A29783; A29783.
DR MIM: 191041; -
DR InterPro: IPR001978; Troponin.
DR Pfam: PF00992; Troponin: 1.
KW Muscle protein; Phosphorylation; Alternative splicing;
KM Multigene family.
FT INIT_MET 0 0
FT MOD_RES 1 1
FT VARSPIC 24 34
FT VARSPIC 204 219
FT CONFLICT 19 19
FT SEQUENCE 277 AA; 32817 MW; 4064FC1F359E63D CRC64;

Query Match 2.1%; Score 7; DB 1; Length 277;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 PEPVAP 181
DB 28 PEPVAP 34

RESULT 14
ALF_MYCGE
ID ALF_MYCGE STANDARD; PRT; 288 AA.
AC P47269;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Fructose-bisphosphate aldolase (EC 4.1.2.13).

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GN FBA OR TSR OR MG023.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
RA Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.-F., Dougherty B.A., Boff K.F., Hu P.-C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal genome complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).
CC -1- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
CC phosphate + D-glyceraldehyde 3-phosphate.
CC -1- COFACTOR: ZINC (BY SIMILARITY).
CC -1- PATHWAY: SIXTH STEP IN GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO CLASS II FRUCTOSE-BISPHOSPHATE ALDOLASE
CC FAMILY.
CC
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CC -----
DR EMBL: U39681; AAC71239.1; -
DR HSSP: P11604; 1ZEN.
DR TIGR: MG023; -
DR InterPro: IPR000771; F_bp-aldolase.
DR Pfam: PF01116; F_bp-aldolase; 1.
DR PROSITE: PS00602; ALDOLASE_CLASS_II_1; 1.
DR PROSITE: PS00806; ALDOLASE_CLASS_II_2; 1.
KW Lyase; Glycolysis; Zinc; Complete proteome.
FT METAL 82 85
FT METAL 85 85
FT SEQUENCE 288 AA; 31310 MW; BD09F4683DD6A32F CRC64;

Query Match 2.1%; Score 7; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 NEKLMQ 287
DB 4 NEKLMQ 10

RESULT 15
ZIPA_PSEAE
ID ZIPA_PSEAE STANDARD; PRT; 289 AA.
AC Q91315;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cell division protein zipa homolog.
DE ZIPA OR PA1528.
GN ZIPA OR PA1528.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043;
DE Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,

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RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Collier L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -I- FUNCTION: Interacts directly with the cell division protein ftsZ.
CC Probable receptor for the septal ring structure, may anchor it
CC to the inner-membrane (By similarity).
CC -I- SUBCELLULAR LOCATION: Type IB membrane protein. Inner membrane (By
CC similarity).
CC -I- SIMILARITY: BELONGS TO THE ZIPA FAMILY.
CC -----
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CC -----
DR EMBL: AE004581; AAG04917.1; -;
DR HSSP: p77173; 1F7X.
KW Cell division; Septation; Transmembrane; Inner membrane;
KW Complete proteome.
FT DOMAIN 1 6 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 7 27 POTENTIAL.
FT DOMAIN 28 289 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 289 AA: 32236 MW: 720D6FED832B329C CRC64;

Query Match 2.1%; Score 7; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 249 VKPGETD 255
| | | | | | | | | |
DB 205 VKPGETD 211

Search completed: September 25, 2002, 09:57:04
Job time: 248 sec

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OM protein - protein search, using sw model

Run on: September 25, 2002, 09:52:41 ; Search time 28.68 Seconds
(without alignments)
1978.464 Million cell updates/sec

Title: us-09-184-826-2
328
Sequence: 1 MMDLRLLILVGAIAIAT.....TPQRLREYODIRREVKDANA 328

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

- 1: SP-archaea:*
- 2: SP-bacteria:*
- 3: SP-fungi:*
- 4: SP-human:*
- 5: SP-invertebrate:*
- 6: SP-mammal:*
- 7: SP-mhc:*
- 8: SP-organella:*
- 9: SP-phage:*
- 10: SP-plant:*
- 11: SP-rodent:*
- 12: SP-virus:*
- 13: SP-vertebrate:*
- 14: SP-unclassified:*
- 15: SP-virus:*
- 16: SP-bacteriap:*
- 17: SP-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9	2.7	137	5	Q20468
2	9	2.7	522	15	Q9WLL1
3	9	2.7	622	15	Q89814
4	8	2.4	130	17	Q9HNM8
5	8	2.4	210	5	Q9XVB2
6	8	2.4	222	2	Q9ADC6
7	8	2.4	234	16	Q92LX9
8	8	2.4	400	5	Q95RV8
9	8	2.4	431	2	Q9S333
10	8	2.4	441	13	Q57311
11	8	2.4	457	10	Q9SSE3
12	8	2.4	512	16	Q9CGA7
13	8	2.4	620	5	Q9VKL0
14	8	2.4	1476	5	Q9YOW1
15	8	2.4	1476	5	Q9YVT4
16	8	2.4	1476	5	Q9NG24

17	8	2.4	2485	5	Q96134	Q96134 plasmidium
18	7	2.1	72	15	P90474	P90474 walleye der
19	7	2.1	72	15	P89225	P89225 walleye der
20	7	2.1	72	15	P89226	P89226 walleye der
21	7	2.1	72	15	P89227	P89227 walleye der
22	7	2.1	72	15	P89228	P89228 walleye der
23	7	2.1	72	15	P89229	P89229 walleye der
24	7	2.1	72	15	P89230	P89230 walleye der
25	7	2.1	72	15	P89231	P89231 walleye der
26	7	2.1	81	5	Q9W500	Q9W500 drosophila
27	7	2.1	82	5	Q9SJD2	Q9SJD2 arabidopsis
28	7	2.1	85	15	Q99DB2	Q99DB2 human immun
29	7	2.1	85	15	Q99DA7	Q99DA7 human immun
30	7	2.1	87	4	Q9U159	Q9U159 homo sapien
31	7	2.1	93	15	Q41565	Q41565 human immun
32	7	2.1	116	12	Q9YJ01	Q9YJ01 african cas
33	7	2.1	116	12	Q9IN46	Q9IN46 south afric
34	7	2.1	120	2	Q93PB7	Q93PB7 microscilla
35	7	2.1	121	2	Q9L5G7	Q9L5G7 salmonella
36	7	2.1	137	15	Q9DRS8	Q9DRS8 human immun
37	7	2.1	144	10	Q9FME9	Q9FME9 arabidopsis
38	7	2.1	148	11	Q35427	Q35427 mus musculu
39	7	2.1	152	15	Q9DRS6	Q9DRS6 human immun
40	7	2.1	162	2	Q9KYB6	Q9KYB6 streptomyce
41	7	2.1	176	5	Q23186	Q23186 caenorhabd1
42	7	2.1	184	15	Q9DRS7	Q9DRS7 human immun
43	7	2.1	186	5	Q16567	Q16567 caenorhabd1
44	7	2.1	187	2	Q9JRL5	Q9JRL5 xanthomonas
45	7	2.1	199	4	Q96A88	Q96A88 homo sapien
46	7	2.1	202	5	Q18903	Q18903 caenorhabd1
47	7	2.1	206	15	Q9DRS9	Q9DRS9 human immun
48	7	2.1	206	15	Q9DRS4	Q9DRS4 human immun
49	7	2.1	212	16	Q9PJ58	Q9PJ58 chlamydia m
50	7	2.1	213	16	Q84471	Q84471 chlamydia t
51	7	2.1	223	5	Q9VLM7	Q9VLM7 drosophila
52	7	2.1	238	9	Q9ZX83	Q9ZX83 bacterioph
53	7	2.1	246	4	Q9BFW8	Q9BFW8 homo sapien
54	7	2.1	246	16	Q51211	Q51211 borrelia bu
55	7	2.1	250	10	Q39956	Q39956 hellianthus
56	7	2.1	252	4	Q9HA13	Q9HA13 homo sapien
57	7	2.1	252	4	Q96A62	Q96A62 homo sapien
58	7	2.1	271	10	Q9FWB9	Q9FWB9 oryza sativ
59	7	2.1	272	16	Q9T118	Q9T118 pseudomonas
60	7	2.1	275	12	Q56822	Q56822 human cytom
61	7	2.1	280	2	Q9ZEE7	Q9ZEE7 lactobacill
62	7	2.1	285	16	Q9XNHO	Q9XNHO streptococ
63	7	2.1	288	5	Q9XYV5	Q9XYV5 toxocara ca
64	7	2.1	290	16	Q91315	Q91315 pseudomonas
65	7	2.1	290	2	Q9RBQ3	Q9RBQ3 xanthomonas
66	7	2.1	290	2	Q9RBQ2	Q9RBQ2 xanthomonas
67	7	2.1	290	2	Q9F238	Q9F238 xanthomonas
68	7	2.1	290	2	Q51899	Q51899 xanthomonas
69	7	2.1	290	10	Q9S7K0	Q9S7K0 oryza sativ
70	7	2.1	290	16	Q9KAU2	Q9KAU2 bacillus ha
71	7	2.1	291	16	Q9KTD2	Q9KTD2 vibrio chol
72	7	2.1	295	2	Q32850	Q32850 mycobacteri
73	7	2.1	309	3	Q9PE61	Q9PE61 schizosacch
74	7	2.1	310	16	Q9KS96	Q9KS96 vibrio chol
75	7	2.1	330	4	Q9Y292	Q9Y292 homo sapien
76	7	2.1	340	4	Q96AT8	Q96AT8 homo sapien
77	7	2.1	343	10	Q9YCJ2	Q9YCJ2 aecoryrum p
78	7	2.1	343	10	Q9AUM7	Q9AUM7 oryza sativ
79	7	2.1	346	16	Q9BFL9	Q9BFL9 rhizobium l
80	7	2.1	355	5	Q9NGO7	Q9NGO7 ostrinia nu
81	7	2.1	356	12	Q88524	Q88524 turkey herp
82	7	2.1	356	16	Q9PA12	Q9PA12 xyella fas
83	7	2.1	358	16	Q9JY93	Q9JY93 neisseria m
84	7	2.1	358	16	Q9J775	Q9J775 neisseria m
85	7	2.1	361	5	Q9W1P2	Q9W1P2 drosophila
86	7	2.1	364	11	Q70509	Q70509 rattus norv
87	7	2.1	365	11	Q99J14	Q99J14 mus musculu
88	7	2.1	372	3	Q9UJ01	Q9UJ01 schizosacch
89	7	2.1	396	16	Q9UCV1	Q9UCV1 lactococcus
90	7	2.1	396	17	Q9V2R1	Q9V2R1 pyrococcus

90	7	2.1	404	16	099W82	099W82 staphylococ	163	7	2.1	2274	5	Q9VYU0	Q9VYU0 drosophila
91	7	2.1	412	2	052939	052939 rhizobium m	164	7	2.1	2777	10	Q9C7S8	Q9C7S8 arabidopsis
92	7	2.1	422	2	Q9R350	Q9R350 streptomyces	165	7	2.1	2977	5	Q9VAP9	Q9VAP9 drosophila
93	7	2.1	440	12	Q9Q6P7	Q9Q6P7 grapevine 1	166	7	2.1	4290	2	Q9WXC0	Q9WXC0 micromosp
94	7	2.1	445	16	Q9CP12	Q9CP12 pasteurella	167	7	2.1	5476	5	Q9NUJ7	Q9NUJ7 drosophila
95	7	2.1	455	5	061747	061747 caenorhabdi	168	7	2.1	5533	5	Q9UCG3	Q9UCG3 drosophila
96	7	2.1	461	8	Q33748	Q33748 arabia ltx	169	7	2.1	5533	5	Q9VPL2	Q9VPL2 drosophila
97	7	2.1	467	4	Q9NX11	Q9NX11 homo sapien	170	7	2.1	5534	5	Q9VNH1	Q9VNH1 drosophila
98	7	2.1	485	5	045265	045265 caenorhabdi	171	7	2.1	5560	5	Q9VPL1	Q9VPL1 drosophila
99	7	2.1	489	16	Q984Y5	Q984Y5 rhizobium 1	172	6	1.8	18	12	Q9IBM7	Q9IBM7 autographa
100	7	2.1	502	16	Q9RS41	Q9RS41 deinococcus	173	6	1.8	24	13	Q9PSR8	Q9PSR8 gallus gall
101	7	2.1	523	17	Q970N4	Q970N4 sulfobolus	174	6	1.8	26	10	Q9S907	Q9S907 avena sativ
102	7	2.1	535	2	Q59813	Q59813 streptomyces	175	6	1.8	38	10	Q9ARK2	Q9ARK2 paenonia lac
103	7	2.1	540	10	Q9FJ30	Q9FJ30 arabidopsis	176	6	1.8	39	9	Q9ARK2	Q9ARK2 paenonia lac
104	7	2.1	548	16	006404	006404 mycobacteri	177	6	1.8	39	10	Q9ARK2	Q9ARK2 paenonia lac
105	7	2.1	551	2	Q9KZS2	Q9KZS2 streptomyces	178	6	1.8	39	16	Q9ARK7	Q9ARK7 paenonia lac
106	7	2.1	552	3	Q9UVB9	Q9UVB9 pichia cife	179	6	1.8	40	10	Q9ARK7	Q9ARK7 paenonia lac
107	7	2.1	552	5	002054	002054 caenorhabdi	180	6	1.8	40	10	Q9ARK5	Q9ARK5 paenonia lac
108	7	2.1	579	11	Q9QZ43	Q9QZ43 mus musculi	181	6	1.8	40	10	Q9ARK5	Q9ARK5 paenonia lac
109	7	2.1	586	4	Q9UCR9	Q9UCR9 homo sapien	182	6	1.8	41	10	Q9ARK5	Q9ARK5 paenonia lac
110	7	2.1	609	10	Q9XG44	Q9XG44 spermatozop	183	6	1.8	41	10	Q9ARK5	Q9ARK5 paenonia lac
111	7	2.1	609	16	Q9A6T7	Q9A6T7 caulobacter	184	6	1.8	41	10	Q9ARK5	Q9ARK5 paenonia lac
112	7	2.1	614	10	Q94EV3	Q94EV3 lycopersico	185	6	1.8	41	10	Q9ARK5	Q9ARK5 paenonia lac
113	7	2.1	615	5	P91573	P91573 caenorhabdi	186	6	1.8	42	10	Q9ARK5	Q9ARK5 paenonia lac
114	7	2.1	638	16	Q988L4	Q988L4 rhizobium 1	187	6	1.8	43	10	Q9ARK8	Q9ARK8 paenonia lac
115	7	2.1	644	5	Q9N4W3	Q9N4W3 caenorhabdi	188	6	1.8	44	2	Q9ZFC8	Q9ZFC8 paenonia lac
116	7	2.1	654	10	Q9LIW2	Q9LIW2 oryza sativ	189	6	1.8	44	10	Q9A0X1	Q9A0X1 paenonia lac
117	7	2.1	677	12	Q91DD8	Q91DD8 ebola virus	190	6	1.8	44	10	Q9A0X0	Q9A0X0 paenonia lac
118	7	2.1	693	16	Q9A537	Q9A537 caulobacter	191	6	1.8	44	10	Q9A0W9	Q9A0W9 paenonia lac
119	7	2.1	696	5	Q9VLS3	Q9VLS3 drosophila	192	6	1.8	44	10	Q9A0W8	Q9A0W8 paenonia lac
120	7	2.1	699	11	Q99K46	Q99K46 mus musculi	193	6	1.8	44	10	Q9A0W7	Q9A0W7 paenonia lac
121	7	2.1	707	10	Q9FGU4	Q9FGU4 arabidopsis	194	6	1.8	44	10	Q9A0W6	Q9A0W6 paenonia lac
122	7	2.1	711	4	Q60899	Q60899 homo sapien	195	6	1.8	44	10	Q9A0W5	Q9A0W5 paenonia lac
123	7	2.1	717	4	Q9UMZ7	Q9UMZ7 homo sapien	196	6	1.8	44	10	Q9ARK7	Q9ARK7 paenonia lac
124	7	2.1	717	4	Q9H307	Q9H307 homo sapien	197	6	1.8	44	10	Q9ARK5	Q9ARK5 paenonia lac
125	7	2.1	725	11	Q35691	Q35691 mus musculi	198	6	1.8	44	10	Q9ARK5	Q9ARK5 paenonia lac
126	7	2.1	731	4	Q60433	Q60433 homo sapien	199	6	1.8	44	10	Q9ARK5	Q9ARK5 paenonia lac
127	7	2.1	736	10	Q9ZMB9	Q9ZMB9 arabidopsis	200	6	1.8	44	10	Q9ARK5	Q9ARK5 paenonia lac
128	7	2.1	743	4	Q99738	Q99738 homo sapien	201	6	1.8	44	10	Q9ARK5	Q9ARK5 paenonia lac
129	7	2.1	744	5	Q9G8J1	Q9G8J1 drosophila	202	6	1.8	44	10	Q9ARK5	Q9ARK5 paenonia lac
130	7	2.1	745	17	Q9Y9L3	Q9Y9L3 aeropyrum p	203	6	1.8	44	10	Q9ARK5	Q9ARK5 paenonia lac
131	7	2.1	759	4	Q9BWP7	Q9BWP7 homo sapien	204	6	1.8	50	11	Q9QZJ9	Q9QZJ9 paenonia lac
132	7	2.1	762	16	Q9AB02	Q9AB02 caulobacter	205	6	1.8	52	10	Q9S8R6	Q9S8R6 paenonia lac
133	7	2.1	780	11	Q9OYX8	Q9OYX8 mus musculi	206	6	1.8	53	12	Q9JE44	Q9JE44 human calic
134	7	2.1	780	11	Q98779	Q98779 raltus norv	207	6	1.8	53	12	Q9JA01	Q9JA01 human calic
135	7	2.1	810	5	Q9U4G9	Q9U4G9 drosophila	208	6	1.8	54	4	Q16487	Q16487 human calic
136	7	2.1	812	16	Q98IK0	Q98IK0 rhizobium 1	209	6	1.8	54	5	Q9TAW9	Q9TAW9 human calic
137	7	2.1	829	4	Q9BZK7	Q9BZK7 homo sapien	210	6	1.8	55	11	Q9QZK0	Q9QZK0 paramicum
138	7	2.1	845	4	Q43273	Q43273 homo sapien	211	6	1.8	56	11	Q9QZK0	Q9QZK0 paramicum
139	7	2.1	848	10	Q9LS51	Q9LS51 arabidopsis	212	6	1.8	57	16	Q9V0U6	Q9V0U6 cavia porce
140	7	2.1	854	4	Q9BZK7	Q9BZK7 rhizobium 1	213	6	1.8	57	16	Q9V0U6	Q9V0U6 cavia porce
141	7	2.1	854	4	Q9BZK7	Q9BZK7 rhizobium 1	214	6	1.8	61	2	Q9S316	Q9S316 rhodospheudo
142	7	2.1	879	2	Q9FBJ2	Q9FBJ2 streptomyces	215	6	1.8	63	5	Q9GPH6	Q9GPH6 callosobruc
143	7	2.1	880	5	Q17338	Q17338 caenorhabdi	216	6	1.8	70	16	Q9K9J0	Q9K9J0 bacillus ha
144	7	2.1	885	5	Q9TXR9	Q9TXR9 caenorhabdi	217	6	1.8	71	2	P77799	P77799 rhodocyclus
145	7	2.1	899	16	Q9Z273	Q9Z273 rhizobium m	218	6	1.8	73	16	Q97RA1	Q97RA1 streptococ
146	7	2.1	911	3	Q96UB8	Q96UB8 neurospora	219	6	1.8	74	11	Q9QZK1	Q9QZK1 cavia porce
147	7	2.1	930	5	Q17339	Q17339 caenorhabdi	220	6	1.8	74	16	Q9CJY7	Q9CJY7 pasteurella
148	7	2.1	980	4	Q9NS55	Q9NS55 homo sapien	221	6	1.8	74	17	Q97BS5	Q97BS5 thermoplasm
149	7	2.1	1045	4	Q9NS56	Q9NS56 homo sapien	222	6	1.8	75	4	Q9UDV4	Q9UDV4 homo sapien
150	7	2.1	1045	4	Q9NS56	Q9NS56 homo sapien	223	6	1.8	75	10	Q941N5	Q941N5 phytoptnor
151	7	2.1	1049	5	Q9UNR9	Q9UNR9 homo sapien	224	6	1.8	75	16	Q928Y4	Q928Y4 listeria in
152	7	2.1	1123	2	Q9VJ14	Q9VJ14 drosophila	225	6	1.8	77	6	P79199	P79199 oviss aries
153	7	2.1	1123	2	Q9VJ14	Q9VJ14 drosophila	226	6	1.8	79	2	Q9AEV9	Q9AEV9 lactococcus
154	7	2.1	1123	2	Q9VJ14	Q9VJ14 drosophila	227	6	1.8	79	5	Q9NE77	Q9NE77 leishmania
155	7	2.1	1233	5	Q9WGV6	Q9WGV6 drosophila	228	6	1.8	80	16	Q9A174	Q9A174 streptococ
156	7	2.1	1306	11	Q9UK31	Q9UK31 mus musculi	229	6	1.8	82	6	Q46622	Q46622 ceratoltheri
157	7	2.1	1362	4	Q96PD3	Q96PD3 homo sapien	230	6	1.8	87	12	Q9QZT9	Q9QZT9 norwalk-11k
158	7	2.1	1420	3	Q13736	Q13736 schizosacch	231	6	1.8	88	10	Q93H60	Q93H60 streptomyces
159	7	2.1	1448	16	Q9HYW9	Q9HYW9 pseudomonas	232	6	1.8	88	10	Q93YI8	Q93YI8 brassica ju
160	7	2.1	1586	13	Q9DFB7	Q9DFB7 gallus gall	233	6	1.8	88	12	Q911T6	Q911T6 rabies viru
161	7	2.1					234	6	1.8				
162	7	2.1					235	6	1.8				

236	6	1.8	88	15	076016	076016 human immun	309	6	1.8	134	16	09JZM1	09JZM1 neisseria m
237	6	1.8	90	15	041568	041568 human immun	310	6	1.8	135	5	09NCN9	09NCN9 giardia lam
238	6	1.8	90	16	09RWZ8	09RWZ8 delnoccocus	311	6	1.8	135	16	005840	005840 mycobacteri
239	6	1.8	91	6	09GM24	09GM24 macaca fasc	312	6	1.8	136	10	09LWZ7	09LWZ7 arabidopsis
240	6	1.8	91	12	09SM16	09SM16 paramecium	313	6	1.8	136	16	09LWZ7	09LWZ7 arabidopsis
241	6	1.8	92	12	051557	051557 pseudomonas	314	6	1.8	137	2	09PBM4	09PBM4 streptomyce
242	6	1.8	92	16	09XZ16	09XZ16 thermocoga	315	6	1.8	137	5	09NCK9	09NCK9 streptomyce
243	6	1.8	92	17	09YAL1	09YAL1 aeropyrum p	316	6	1.8	138	5	09NCK7	09NCK7 drosophila
244	6	1.8	94	16	09PH45	09PH45 xylella fas	317	6	1.8	138	5	09NCK7	09NCK7 drosophila
245	6	1.8	96	2	051612	051612 unidentified	318	6	1.8	138	10	09ADU2	09ADU2 oryza sativ
246	6	1.8	96	15	040298	040298 human immun	319	6	1.8	138	16	09ZVU3	09ZVU3 rhizobium m
247	6	1.8	97	16	053672	053672 mycobacteri	320	6	1.8	138	17	09ZVU3	09ZVU3 rhizobium m
248	6	1.8	97	16	09XK37	09XK37 rhizobium l	321	6	1.8	139	4	09BST1	09BST1 homo saplen
249	6	1.8	98	16	069509	069509 mycobacteri	322	6	1.8	139	4	09NMK0	09NMK0 homo saplen
250	6	1.8	100	16	09XBE4	09XBE4 streptomyce	323	6	1.8	139	16	09JUC5	09JUC5 neisseria m
251	6	1.8	100	17	09PLT4	09PLT4 chlamydia m	324	6	1.8	139	16	09JUC5	09JUC5 neisseria m
252	6	1.8	100	17	09YDM4	09YDM4 aeropyrum p	325	6	1.8	141	4	09NXX4	09NXX4 homo saplen
253	6	1.8	101	10	09ARA4	09ARA4 linum usita	326	6	1.8	141	17	09ZVU3	09ZVU3 rhizobium m
254	6	1.8	102	2	09ROY9	09ROY9 mycobacteri	327	6	1.8	143	16	09ZCF0	09ZCF0 rickettsia
255	6	1.8	102	16	0969J3	0969J3 rhizobium l	328	6	1.8	143	16	09ZCF0	09ZCF0 rickettsia
256	6	1.8	103	16	09PDN9	09PDN9 xylella fas	329	6	1.8	144	2	09RNG3	09RNG3 mycobacteri
257	6	1.8	104	2	09KSH9	09KSH9 bordetella	330	6	1.8	144	2	052206	052206 morganella
258	6	1.8	105	2	09KSH7	09KSH7 bordetella	331	6	1.8	144	2	052210	052210 serralia ma
259	6	1.8	105	2	09KSG5	09KSG5 bordetella	332	6	1.8	144	10	09LJ53	09LJ53 arabidopsis
260	6	1.8	105	3	09Y7H2	09Y7H2 plitomyces s	333	6	1.8	145	17	09HNP4	09HNP4 halobacteri
261	6	1.8	105	8	09XOR1	09XOR1 oryza sativ	334	6	1.8	146	11	060482	060482 cavia porce
262	6	1.8	105	8	09YJ57	09YJ57 oryza sativ	335	6	1.8	147	1	09C4V2	09C4V2 sulfolobus
263	6	1.8	105	8	09YJ57	09YJ57 oryza sativ	336	6	1.8	147	1	09C4V2	09C4V2 sulfolobus
264	6	1.8	105	8	09YJ57	09YJ57 oryza sativ	337	6	1.8	147	11	09C4V2	09C4V2 sulfolobus
265	6	1.8	105	8	09YJ57	09YJ57 oryza sativ	338	6	1.8	147	11	09C4V2	09C4V2 sulfolobus
266	6	1.8	107	2	09R3B4	09R3B4 pseudomonas	339	6	1.8	147	11	09C4V2	09C4V2 sulfolobus
267	6	1.8	107	2	09KSH5	09KSH5 bordetella	340	6	1.8	147	11	09C4V2	09C4V2 sulfolobus
268	6	1.8	107	2	09KSH5	09KSH5 bordetella	341	6	1.8	147	11	09C4V2	09C4V2 sulfolobus
269	6	1.8	107	2	09KSH5	09KSH5 bordetella	342	6	1.8	148	1	09YF58	09YF58 aeropyrum p
270	6	1.8	108	10	083328	083328 arabidopsis	343	6	1.8	148	2	066226	066226 synechococ
271	6	1.8	109	2	09AJH0	09AJH0 vibrio prot	344	6	1.8	148	4	075575	075575 homo saplen
272	6	1.8	109	2	09KSH1	09KSH1 bordetella	345	6	1.8	148	10	02A162	02A162 nicotiana t
273	6	1.8	109	6	09BE33	09BE33 macaca fasc	346	6	1.8	148	17	09W026	09W026 pyrococcus
274	6	1.8	110	6	09TUL1	09TUL1 macaca mula	347	6	1.8	150	5	09W026	09W026 pyrococcus
275	6	1.8	110	12	09IR98	09IR98 japanese lr	348	6	1.8	151	16	09KLP9	09KLP9 vibrio chol
276	6	1.8	110	17	09YCL0	09YCL0 aeropyrum p	349	6	1.8	151	16	09KLP9	09KLP9 pseudomonas
277	6	1.8	111	2	09KSG9	09KSG9 bordetella	350	6	1.8	152	2	052578	052578 agrobacteri
278	6	1.8	112	16	09KSG7	09KSG7 bordetella	351	6	1.8	152	2	052592	052592 agrobacteri
279	6	1.8	112	17	09YEH9	09YEH9 streptococ	352	6	1.8	155	2	09YU03	09YU03 escherichia
280	6	1.8	115	2	09KJY1	09KJY1 aeropyrum p	353	6	1.8	155	2	09YU03	09YU03 escherichia
281	6	1.8	115	2	09KJY1	09KJY1 bordetella	354	6	1.8	155	4	09P0R6	09P0R6 neisseria m
282	6	1.8	115	2	09KJY1	09KJY1 bordetella	355	6	1.8	155	11	070440	070440 mus muscu
283	6	1.8	115	2	09KJY1	09KJY1 bordetella	356	6	1.8	155	12	086797	086797 turkay herp
284	6	1.8	116	5	09GR25	09GR25 nematostell	357	6	1.8	155	12	069310	069310 schizosacch
285	6	1.8	116	5	09BN62	09BN62 prosocolem	358	6	1.8	156	3	09P7J9	09P7J9 caenorhabd
286	6	1.8	117	12	09J4J8	09J4J8 sulfolobus	359	6	1.8	156	3	09P7J9	09P7J9 caenorhabd
287	6	1.8	117	5	09W398	09W398 drosophila	360	6	1.8	156	8	09TLV7	09TLV7 cyanidulum c
288	6	1.8	117	16	032022	032022 bacillus su	361	6	1.8	157	2	047443	047443 escherichia
289	6	1.8	118	9	09ZK36	09ZK36 mycobacteri	362	6	1.8	158	10	094023	094023 arabidopsis
290	6	1.8	118	15	076140	076140 human immun	363	6	1.8	159	5	09VIL5	09VIL5 drosophila
291	6	1.8	118	16	09RV14	09RV14 delnoccocus	364	6	1.8	159	10	09LFF40	09LFF40 arabidopsis
292	6	1.8	122	2	09KJX9	09KJX9 bordetella	365	6	1.8	160	5	094443	094443 chironomus
293	6	1.8	122	2	09KJX9	09KJX9 bordetella	366	6	1.8	160	11	09Q278	09Q278 chironomus
294	6	1.8	124	2	09R7L2	09R7L2 bacillus su	367	6	1.8	160	16	09ZWL4	09ZWL4 cavia sp. p
295	6	1.8	124	4	09R7L1	09R7L1 unidentified	368	6	1.8	160	16	09ZWL4	09ZWL4 cavia sp. p
296	6	1.8	124	4	09R7L1	09R7L1 unidentified	369	6	1.8	161	17	0980M4	0980M4 sulfolobus
297	6	1.8	127	15	09QMSV5	09QMSV5 acetabulari	370	6	1.8	161	2	030617	030617 myxococcus
298	6	1.8	127	15	09QMSV5	09QMSV5 acetabulari	371	6	1.8	161	5	002368	002368 chironomus
299	6	1.8	127	16	09JXK0	09JXK0 human immun	372	6	1.8	161	16	09FBC1	09FBC1 streptococ
300	6	1.8	127	16	09JXK0	09JXK0 human immun	373	6	1.8	161	16	09FBC1	09FBC1 streptococ
301	6	1.8	128	5	061215	061215 caenorhabd	374	6	1.8	162	5	09Z9W5	09Z9W5 koefflerius
302	6	1.8	128	5	061215	061215 caenorhabd	375	6	1.8	162	5	09Z9W5	09Z9W5 koefflerius
303	6	1.8	129	15	09NVV2	09NVV2 human immun	376	6	1.8	163	5	09L559	09L559 pseudomonas
304	6	1.8	129	15	09NVV2	09NVV2 human immun	377	6	1.8	163	5	09L559	09L559 pseudomonas
305	6	1.8	131	2	09ZP99	09ZP99 listeria in	378	6	1.8	163	5	045848	045848 caenorhabd
306	6	1.8	132	12	041075	041075 paramecium	379	6	1.8	164	4	09CXZ2	09CXZ2 mus muscu
307	6	1.8	134	2	09F5F1	09F5F1 agrobacteri	380	6	1.8	164	4	09NV35	09NV35 homo saplen
308	6	1.8	134	11	09CRZ2	09CRZ2 mus muscu	381	6	1.8	164	9	09MCD9	09MCD9 bacterioph

382	1.8	165	8	Q950T3	Q950C3 hyaloraphid	455	6	1.8	198	2	Q9AHP0	Q9AHP0 bordetella
383	1.8	165	6	Q981V8	Q981V8 rhizobium l	456	6	1.8	198	10	Q9C7Y9	Q9C7Y9 arabidopsis
384	1.8	165	17	Q96YF0	Q96YF0 sulfolobus	457	6	1.8	199	10	Q9SFU5	Q9SFU5 arabidopsis
385	1.8	166	2	Q9Z1M5	Q9Z1M5 listeria mo	458	6	1.8	200	2	Q9RK54	Q9RK54 streptomyce
386	1.8	166	4	Q9H8L8	Q9H8L8 homo sapien	459	6	1.8	200	2	Q9ALP9	Q9ALP9 bordetella
387	1.8	166	10	Q9FCAS	Q9FCAS arabidopsis	460	6	1.8	200	12	Q9DJ41	Q9DJ41 spodoptera
388	1.8	166	16	Q9Z8N5	Q9Z8N5 listeria in	461	6	1.8	200	16	Q9A6T1	Q9A6T1 caulobacter
389	1.8	167	16	Q9PAS8	Q9PAS8 xylella fas	462	6	1.8	202	17	Q97J53	Q97J53 caulobacter
390	1.8	168	2	Q9S6K2	Q9S6K2 campylobact	463	6	1.8	203	4	Q96GR5	Q96GR5 homo sapien
391	1.8	168	10	Q9XFP6	Q9XFP6 prunus arme	464	6	1.8	203	5	Q180J6	Q180J6 caenorhabdi
392	1.8	168	10	Q9SM77	Q9SM77 oryza sativ	465	6	1.8	203	10	Q9SFU7	Q9SFU7 arabidopsis
393	1.8	168	16	Q9Z8T5	Q9Z8T5 rhizobium m	466	6	1.8	203	16	Q9PLJ4	Q9PLJ4 campylobact
394	1.8	169	11	Q646I4	Q646I4 rattus norv	467	6	1.8	204	8	Q37397	Q37397 allomyces m
395	1.8	169	16	Q9K7E0	Q9K7E0 bacillus ha	468	6	1.8	204	12	Q9ICG6	Q9ICG6 white spot
396	1.8	170	4	Q9BWS8	Q9BWS8 homo sapien	469	6	1.8	204	13	Q13J25	Q13J25 poeciliopst
397	1.8	170	4	Q9P0M6	Q9P0M6 homo sapien	470	6	1.8	205	17	Q9VJW7	Q9VJW7 pyrococcus
398	1.8	170	10	Q9SYP8	Q9SYP8 arabidopsis	471	6	1.8	206	4	Q96VY2	Q96VY2 homo sapien
399	1.8	172	10	Q80393	Q80393 mesembryant	472	6	1.8	208	10	Q9LXM3	Q9LXM3 arabidopsis
400	1.8	172	13	Q919J6	Q919J6 gallus gall	473	6	1.8	208	16	Q9PER6	Q9PER6 xylella fas
401	1.8	172	13	Q90368	Q90368 coturnix gall	474	6	1.8	209	2	Q9L593	Q9L593 streptococc
402	1.8	173	10	Q9M4H7	Q9M4H7 vitis vinif	475	6	1.8	212	11	Q9CRJ0	Q9CRJ0 mus muscicu
403	1.8	173	5	Q201J8	Q201J8 caenorhabdi	476	6	1.8	213	2	Q9X6F5	Q9X6F5 campylobact
404	1.8	175	10	Q230I1	Q230I1 arabidopsis	477	6	1.8	213	2	Q9X6F6	Q9X6F6 campylobact
405	1.8	175	10	Q230I1	Q230I1 mus muscicu	478	6	1.8	213	5	Q9GTY8	Q9GTY8 campylobact
406	1.8	176	11	Q883I2	Q883I2 mus muscicu	479	6	1.8	213	10	Q9C782	Q9C782 arabidopsis
407	1.8	176	11	Q9JUT3	Q9JUT3 mus muscicu	480	6	1.8	213	11	Q9D3J8	Q9D3J8 mus muscicu
408	1.8	176	16	Q9BDU4	Q9BDU4 rhizobium l	481	6	1.8	214	16	Q91234	Q91234 pseudomonas
409	1.8	177	10	Q9AS02	Q9AS02 oryza sativ	482	6	1.8	214	11	Q9R008	Q9R008 mus muscicu
410	1.8	178	5	Q9BH30	Q9BH30 bombyx mori	483	6	1.8	215	2	Q91PQ3	Q91PQ3 tt virus. o
411	1.8	178	11	Q9OZ87	Q9OZ87 mus muscicu	484	6	1.8	215	12	Q9ALQ4	Q9ALQ4 bordetella
412	1.8	180	17	Q9YDP6	Q9YDP6 aetopyrum p	485	6	1.8	215	16	Q9RTH9	Q9RTH9 delnococtus
413	1.8	180	17	Q979H7	Q979H7 thermoplasma	486	6	1.8	215	16	Q9HMH2	Q9HMH2 sus scrofa
414	1.8	181	5	Q440Y3	Q440Y3 drosophila	487	6	1.8	216	6	Q9BDH3	Q9BDH3 sus scrofa
415	1.8	181	16	Q91341	Q91341 pseudomonas	488	6	1.8	216	17	Q9HMH2	Q9HMH2 sus scrofa
416	1.8	182	5	Q95R29	Q95R29 mus muscicu	489	6	1.8	216	11	Q9D440	Q9D440 mus muscicu
417	1.8	183	11	Q9CMA7	Q9CMA7 human immun	490	6	1.8	216	12	Q9C0C2	Q9C0C2 simian cyto
418	1.8	183	15	Q9CCO4	Q9CCO4 chrysodidym	491	6	1.8	216	16	Q97M23	Q97M23 clostridium
419	1.8	184	8	Q9KGB6	Q9KGB6 homo sapien	492	6	1.8	217	16	Q9CEW9	Q9CEW9 lactococcus
420	1.8	185	4	Q9HBP9	Q9HBP9 homo sapien	493	6	1.8	217	16	Q99ZG6	Q99ZG6 streptococc
421	1.8	185	5	P91455	P91455 caenorhabdi	494	6	1.8	217	16	Q97Q36	Q97Q36 streptococc
422	1.8	186	2	Q9Z667	Q9Z667 zymomonas m	495	6	1.8	218	17	Q975M7	Q975M7 sulfolobus
423	1.8	186	10	Q9LID5	Q9LID5 arabidopsis	496	6	1.8	219	5	Q96ZU1	Q96ZU1 spodoptera
424	1.8	187	2	Q9JRM0	Q9JRM0 xanthomonas	497	6	1.8	219	10	Q9ZTW3	Q9ZTW3 arabidopsis
425	1.8	187	2	Q9JRL9	Q9JRL9 xanthomonas	498	6	1.8	219	14	Q91US0	Q91US0 plasmid psb
426	1.8	187	2	Q9JRL8	Q9JRL8 xanthomonas	499	6	1.8	219	16	Q9A2Y3	Q9A2Y3 caulobacter
427	1.8	187	2	Q9JRL7	Q9JRL7 xanthomonas	500	6	1.8	219	17	Q9V1Z4	Q9V1Z4 pyrococcus
428	1.8	187	10	Q9M692	Q9M692 gossypioide	501	6	1.8	221	5	Q9NEU2	Q9NEU2 caenorhabdi
429	1.8	188	2	Q9S691	Q9S691 haemophilus	502	6	1.8	222	2	Q9LBR2	Q9LBR2 mycobacteri
430	1.8	188	2	Q9S6A5	Q9S6A5 haemophilus	503	6	1.8	222	2	Q9L584	Q9L584 streptococc
431	1.8	188	2	Q9S6A6	Q9S6A6 haemophilus	504	6	1.8	222	2	Q9L577	Q9L577 streptococc
432	1.8	188	2	Q9S6A9	Q9S6A9 haemophilus	505	6	1.8	222	5	Q01786	Q01786 caenorhabdi
433	1.8	188	3	Q9USC5	Q9USC5 schizosacch	506	6	1.8	223	16	Q9A740	Q9A740 caulobacter
434	1.8	189	2	Q9S6A4	Q9S6A4 haemophilus	507	6	1.8	223	17	Q96XAS	Q96XAS sulfolobus
435	1.8	189	16	Q9H2T7	Q9H2T7 pseudomonas	508	6	1.8	224	2	Q9KKH2	Q9KKH2 yersinia en
436	1.8	190	4	Q96ITU	Q96ITU homo sapien	509	6	1.8	224	2	Q9SLI0	Q9SLI0 streptomyce
437	1.8	190	4	Q9ZXB6	Q9ZXB6 bacterioph	510	6	1.8	224	2	Q93NK7	Q93NK7 yersinia en
438	1.8	191	17	Q97Z57	Q97Z57 sulfolobus	511	6	1.8	224	4	Q00309	Q00309 homo sapien
439	1.8	191	16	Q9H2R0	Q9H2R0 homo sapien	512	6	1.8	224	10	Q40760	Q40760 picea abies
440	1.8	191	16	Q9KSL0	Q9KSL0 vibrio chol	513	6	1.8	225	2	Q9L591	Q9L591 streptococc
441	1.8	191	17	Q9YBM4	Q9YBM4 aetopyrum p	514	6	1.8	225	16	Q98PT4	Q98PT4 mycoplasma
442	1.8	192	5	Q9XYT6	Q9XYT6 leishmania	515	6	1.8	226	12	Q98Z60	Q98Z60 mollusca c
443	1.8	193	8	Q935G8	Q935G8 philautes c	516	6	1.8	227	5	Q9KCS0	Q9KCS0 streptococc
444	1.8	194	12	Q943S3	Q943S3 oryza sativ	517	6	1.8	227	5	Q00924	Q00924 plasmodium
445	1.8	194	16	Q04393	Q04393 acholeplasm	518	6	1.8	227	5	Q9CRV7	Q9CRV7 plasmodium
446	1.8	194	16	Q9A105	Q9A105 streptococc	519	6	1.8	227	8	Q986X7	Q986X7 cryptosporid
447	1.8	195	4	Q60532	Q60532 homo sapien	520	6	1.8	227	10	Q94AY4	Q94AY4 arabidopsis
448	1.8	196	12	Q918B7	Q918B7 norway-lik	521	6	1.8	227	16	Q06556	Q06556 mycobacteri
449	1.8	196	12	Q918B1	Q918B1 norway-lik	522	6	1.8	228	2	Q915B8	Q915B8 streptococc
450	1.8	196	12	Q918A8	Q918A8 norway-lik	523	6	1.8	228	8	Q9MLZ5	Q9MLZ5 sceloporus
451	1.8	197	8	Q9S212	Q9S212 streptomyce	524	6	1.8	228	11	Q92357	Q92357 rattus norv
452	1.8	197	8	Q9TBM2	Q9TBM2 acropora te	525	6	1.8	228	16	Q9A306	Q9A306 caulobacter
453	1.8	197	16	Q53706	Q53706 mycobacteri	526	6	1.8	228	16	Q97MP4	Q97MP4 clostridium
454	1.8	197	16	Q9KCU7	Q9KCU7 bacillus ha	527	6	1.8	228	17	Q27259	Q27259 methanother

528	6	1.8	228	17	Q9HSL4	Q9HSL4 halobacteri	601	6	1.8	258	12	Q98444	Q98444 paramecium
529	6	1.8	229	8	Q9MLZ4	Q9MLZ4 sceloporus	602	6	1.8	258	17	Q9264	Q9264 archaeoglob
530	6	1.8	229	16	Q98KC5	Q98KC5 rhizobium 1	603	6	1.8	259	4	Q96EE0	Q96EE0 homo sapien
531	6	1.8	230	16	Q9PB87	Q9PB87 xyella fas	604	6	1.8	260	2	P71102	P71102 curtiobacter
532	6	1.8	231	2	Q06030	Q06030 lactococcus	605	6	1.8	260	2	Q52548	Q52548 pseudomonas
533	6	1.8	231	2	Q9L579	Q9L579 streptococc	606	6	1.8	260	5	Q9VRD1	Q9VRD1 drosophila
534	6	1.8	231	2	Q9ALP3	Q9ALP3 bordetella	607	6	1.8	260	7	Q06744	Q06744 xenopus lae
535	6	1.8	231	8	Q9G5K2	Q9G5K2 anolis mar	608	6	1.8	260	7	Q06746	Q06746 xenopus lae
536	6	1.8	231	8	Q9G5J4	Q9G5J4 anolis mar	609	6	1.8	261	5	Q25240	Q25240 leishmania
537	6	1.8	231	8	Q9G5J3	Q9G5J3 anolis ocul	610	6	1.8	261	5	P91279	P91279 caenorhabd1
538	6	1.8	231	8	Q9G5J2	Q9G5J2 anolis livi	611	6	1.8	261	11	Q9GUP7	Q9GUP7 mus musculu
539	6	1.8	231	10	Q9SNT9	Q9SNT9 oryza sativ	612	6	1.8	261	16	Q9ZAP6	Q9ZAP6 listeria in
540	6	1.8	231	16	Q91079	Q91079 pseudomonas	613	6	1.8	262	2	Q9L576	Q9L576 streptococ
541	6	1.8	232	5	Q16890	Q16890 caenorhabd1	614	6	1.8	262	10	Q9SWC5	Q9SWC5 betula ver
542	6	1.8	232	12	Q08398	Q08398 paramecium	615	6	1.8	262	11	Q08346	Q08346 mus musculu
543	6	1.8	232	16	Q9ZMU1	Q9ZMU1 rhizobium m	616	6	1.8	262	12	Q918P3	Q918P3 bovine harp
544	6	1.8	232	17	Q57773	Q57773 pyrococcus	617	6	1.8	263	3	Q74316	Q74316 schizosacch
545	6	1.8	234	10	Q48529	Q48529 arabidopsis	618	6	1.8	263	5	Q9WVK3	Q9WVK3 drosophila
546	6	1.8	234	16	Q99YB2	Q99YB2 streptococ	619	6	1.8	263	10	Q9LVL9	Q9LVL9 arabidopsi
547	6	1.8	235	2	Q9L582	Q9L582 streptococ	620	6	1.8	264	10	Q9YMT0	Q9YMT0 lymantria d
548	6	1.8	236	2	Q9ZAM2	Q9ZAM2 sphingomona	621	6	1.8	264	16	Q98K02	Q98K02 rhizobium 1
549	6	1.8	237	2	Q9L592	Q9L592 streptococ	622	6	1.8	264	16	P71701	P71701 mycobacteri
550	6	1.8	237	5	Q19860	Q19860 caenorhabd1	623	6	1.8	265	10	Q9LTP9	Q9LTP9 arabidopsi
551	6	1.8	237	16	Q97R52	Q97R52 streptococ	624	6	1.8	266	6	Q95KD6	Q95KD6 macaca fasc
552	6	1.8	238	16	Q66599	Q66599 aquilex aeo	625	6	1.8	266	10	Q9FRF5	Q9FRF5 arabidopsi
553	6	1.8	238	16	Q9K7T6	Q9K7T6 bacillus ha	626	6	1.8	266	10	Q93VE7	Q93VE7 arabidopsi
554	6	1.8	239	2	Q49014	Q49014 mycoplasma	627	6	1.8	266	16	Q9PP58	Q9PP58 campylobact
555	6	1.8	239	16	Q97MW9	Q97MW9 aeropyrum p	628	6	1.8	267	2	Q9RNL1	Q9RNL1 zymomonas m
556	6	1.8	241	17	Q9YAS7	Q9YAS7 aeropyrum p	629	6	1.8	267	2	Q05150	Q05150 rhodococcus
557	6	1.8	241	5	Q9V332	Q9V332 drosophila	630	6	1.8	267	8	Q94W05	Q94W05 pleococcus au
558	6	1.8	241	16	P73234	P73234 synecocyst	631	6	1.8	267	12	Q56823	Q56823 human cytom
559	6	1.8	242	2	Q9L562	Q9L562 streptococ	632	6	1.8	267	12	Q56824	Q56824 human cytom
560	6	1.8	242	2	Q44929	Q44929 bacillus br	633	6	1.8	267	12	Q56825	Q56825 human cytom
561	6	1.8	242	4	Q96N48	Q96N48 homo sapien	634	6	1.8	267	12	Q56829	Q56829 human cytom
562	6	1.8	242	16	Q98FE24	Q98FE24 rhizobium 1	635	6	1.8	267	5	Q26561	Q26561 schistosoma
563	6	1.8	243	10	Q9SDB8	Q9SDB8 oryza sativ	636	6	1.8	268	12	Q56826	Q56826 human cytom
564	6	1.8	243	11	Q61303	Q61303 mus musculu	637	6	1.8	268	16	Q914N2	Q914N2 pseudomonas
565	6	1.8	245	4	Q9UQK7	Q9UQK7 homo sapien	638	6	1.8	269	2	Q9KXC3	Q9KXC3 streptomyc
566	6	1.8	245	12	Q69127	Q69127 human herpe	639	6	1.8	269	2	Q46097	Q46097 campylobact
567	6	1.8	245	16	Q9X101	Q9X101 thermotoga	640	6	1.8	269	7	Q06742	Q06742 xenopus lae
568	6	1.8	245	16	Q9CBA6	Q9CBA6 mycobacteri	641	6	1.8	269	7	Q06743	Q06743 xenopus lae
569	6	1.8	246	2	Q9LSB4	Q9LSB4 streptococ	642	6	1.8	269	8	Q950L8	Q950L8 rhizophydlu
570	6	1.8	246	2	Q9LS78	Q9LS78 streptococ	643	6	1.8	269	17	Q9YBA6	Q9YBA6 aeropyrum p
571	6	1.8	246	6	Q9SLM4	Q9SLM4 macaca fasc	644	6	1.8	270	2	Q9R6V2	Q9R6V2 synecococ
572	6	1.8	247	6	Q9BDH4	Q9BDH4 sus scrofa	645	6	1.8	270	2	Q34158	Q34158 salmonella
573	6	1.8	247	16	Q9L5D4	Q9L5D4 pseudomonas	646	6	1.8	270	3	Q12253	Q12253 saccharomyc
574	6	1.8	249	2	Q9L5B7	Q9L5B7 streptococ	647	6	1.8	270	7	Q06745	Q06745 xenopus lae
575	6	1.8	249	2	Q9L585	Q9L585 streptococ	648	6	1.8	270	11	Q9D8G2	Q9D8G2 mus musculu
576	6	1.8	249	3	Q06672	Q06672 saccharomyc	649	6	1.8	271	5	Q9UID5	Q9UID5 leishmania
577	6	1.8	250	4	Q9B058	Q9B058 rhizobium 1	650	6	1.8	271	16	Q916U7	Q916U7 pseudomonas
578	6	1.8	250	5	Q9VKG7	Q9VKG7 homo sapien	651	6	1.8	271	16	Q98JG9	Q98JG9 rhizobium 1
579	6	1.8	251	4	Q9NKA0	Q9NKA0 homo sapien	652	6	1.8	272	4	Q9BWR0	Q9BWR0 homo sapien
580	6	1.8	251	10	Q49473	Q49473 arabidopsi	653	6	1.8	272	5	Q9BWT6	Q9BWT6 sarcia sp.
581	6	1.8	252	2	Q9L583	Q9L583 streptococ	654	6	1.8	272	12	Q56827	Q56827 human cytom
582	6	1.8	252	2	Q9ALQ2	Q9ALQ2 bordetella	655	6	1.8	273	5	Q95Y76	Q95Y76 caenorhabd1
583	6	1.8	253	2	P94626	P94626 clostridium	656	6	1.8	273	16	Q9K0I1	Q9K0I1 neisseria m
584	6	1.8	253	10	Q22082	Q22082 petunia hyb	657	6	1.8	273	16	Q9JVI4	Q9JVI4 neisseria m
585	6	1.8	253	11	Q9DBJ0	Q9DBJ0 mus musculu	658	6	1.8	273	17	Q58086	Q58086 pyrococcus
586	6	1.8	253	16	P94382	P94382 bacillus su	659	6	1.8	273	17	Q9HRP4	Q9HRP4 halobacteri
587	6	1.8	253	17	Q27406	Q27406 methanother	660	6	1.8	274	16	Q9HYG4	Q9HYG4 pseudomonas
588	6	1.8	254	4	Q60768	Q60768 homo sapien	661	6	1.8	274	3	P78840	P78840 schizosacch
589	6	1.8	254	4	Q9K3Y6	Q9K3Y6 streptomyc	662	6	1.8	275	3	Q9UC3	Q9UC3 caenorhabd1
590	6	1.8	255	2	Q9L5B6	Q9L5B6 streptococ	663	6	1.8	275	5	Q9UC3	Q9UC3 schizosacch
591	6	1.8	255	2	Q9L581	Q9L581 streptococ	664	6	1.8	275	5	Q9XW88	Q9XW88 caenorhabd1
592	6	1.8	256	2	Q9L595	Q9L595 streptococ	665	6	1.8	275	11	Q9JLE2	Q9JLE2 mus musculu
593	6	1.8	256	2	Q9ALQ0	Q9ALQ0 bordetella	666	6	1.8	276	5	Q9VHM6	Q9VHM6 alcelaphine
594	6	1.8	256	16	Q9L594	Q9L594 rhizobium 1	667	6	1.8	276	16	Q9ZV63	Q9ZV63 rhizobium m
595	6	1.8	257	2	Q9L594	Q9L594 streptococ	668	6	1.8	277	5	Q9NET3	Q9NET3 caenorhabd1
596	6	1.8	257	16	Q99Y11	Q99Y11 streptococ	669	6	1.8	277	5	Q27045	Q27045 theileria p
597	6	1.8	257	16	Q99Y11	Q99Y11 streptococ	670	6	1.8	278	16	Q9HTB1	Q9HTB1 pseudomonas
598	6	1.8	257	16	Q99Y11	Q99Y11 streptococ	671	6	1.8				
599	6	1.8	257	16	Q99Y11	Q99Y11 streptococ	672	6	1.8				
600	6	1.8	257	16	Q99Y11	Q99Y11 streptococ	673	6	1.8				

674	6	1.8	280	10	Q94I08	Q94Iq8 oryza sativ	747	6	1.8	307	2	P95407	P95407 pseudomonas
675	6	1.8	281	4	Q96P12	Q96p12 homo sapien	748	6	1.8	307	2	Q59709	Q59709 pseudomonas
676	6	1.8	281	16	Q84203	Q84203 chlamydia t	749	6	1.8	307	2	Q59708	Q59708 pseudomonas
677	6	1.8	284	11	Q9C2L3	Q9c2l3 mus musculu	750	6	1.8	307	10	Q9AY72	Q9ay72 oryza sativ
678	6	1.8	284	16	Q9K6I3	Q9k6i3 bacillus ha	751	6	1.8	307	10	Q9W030	Q9w030 arabidopsis
679	6	1.8	285	5	Q17453	Q17453 caenorhabdi	752	6	1.8	307	10	Q9CEX6	Q9ceX6 lactococcus
680	6	1.8	285	11	Q9CY28	Q9cy28 mus musculu	753	6	1.8	307	16	Q9CEX6	Q9ceX6 lactococcus
681	6	1.8	286	5	Q9GUJ6	Q9guj6 trypanosoma	754	6	1.8	307	17	Q28263	Q28263 archaeoglob
682	6	1.8	286	16	Q9CKX6	Q9ckx6 pasteurella	755	6	1.8	308	10	Q9MA06	Q9ma06 arabidopsis
683	6	1.8	286	16	Q9CCW1	Q9ccw1 mycobacteri	756	6	1.8	309	2	Q87625	Q87625 pseudomonas
684	6	1.8	287	2	Q9RLJ6	Q9rlj6 oenococcus	757	6	1.8	309	10	Q9SSR0	Q9ssr0 arabidopsis
685	6	1.8	287	2	Q9RLJ5	Q9rlj5 oenococcus	758	6	1.8	310	4	Q96SG6	Q96sg6 homo sapien
686	6	1.8	287	13	Q930X1	Q93qx1 corynebacte	759	6	1.8	310	13	Q98T56	Q98t56 tockus eryt
687	6	1.8	287	13	Q91002	Q91002 gallus gall	760	6	1.8	310	17	Q9UXJ4	Q9uxj4 sulfobolus
688	6	1.8	287	16	Q9PKJ2	Q9pkj2 chlamydia m	761	6	1.8	311	5	Q9NF49	Q9nf49 drosophila
689	6	1.8	288	3	Q9K430	Q9k430 saccharomyc	762	6	1.8	311	10	Q9FTT1	Q9ftt1 oryza sativ
690	6	1.8	288	5	Q9MI04	Q9mi04 drosophila	763	6	1.8	311	12	Q91GCA	Q91gca oryza sativ
691	6	1.8	288	12	Q91GT9	Q91gt9 porcine ade	764	6	1.8	311	16	Q9ZSW2	Q9zsw2 epiphyas po
692	6	1.8	289	2	Q9K273	Q9k273 streptomyc	765	6	1.8	312	5	Q76577	Q76577 caenorhabdi
693	6	1.8	289	2	Q9K273	Q9k273 streptomyc	766	6	1.8	312	11	Q9CWP4	Q9cwp4 mus musculu
694	6	1.8	289	12	Q91H10	Q91h10 human calic	767	6	1.8	312	15	Q98CQ9	Q98cq9 rhizobium l
695	6	1.8	290	12	Q89483	Q89483 gallid herp	768	6	1.8	313	5	Q95SU6	Q95su6 drosophila
696	6	1.8	290	12	Q86876	Q86876 gallid herp	769	6	1.8	314	8	Q9MD53	Q9md53 phytomonas
697	6	1.8	290	12	Q69304	Q69304 marek's dis	770	6	1.8	314	11	Q9EPG2	Q9epg2 mus musculu
698	6	1.8	291	2	Q9K4G6	Q9k4g6 streptomyc	771	6	1.8	315	6	Q97601	Q97601 oryctolagus
699	6	1.8	291	2	Q93TU0	Q93tu0 acidithioba	772	6	1.8	316	2	Q9AE41	Q9ae41 rhizobium l
700	6	1.8	291	11	Q91XF6	Q91xf6 mus musculu	773	6	1.8	316	5	Q9VC37	Q9vc37 drosophila
701	6	1.8	291	16	Q9CL10	Q9cl10 pasteurella	774	6	1.8	316	5	Q95PB3	Q95pb3 ascaris suu
702	6	1.8	291	16	Q929F4	Q929f4 listeria in	775	6	1.8	316	10	Q91J12	Q91j12 arabidopsis
703	6	1.8	291	17	Q96X95	Q96x95 sulfobolus	776	6	1.8	316	10	P93323	P93323 medicago sa
704	6	1.8	292	3	Q96WPI	Q96wpi agaricus bi	777	6	1.8	317	5	Q95PB5	Q95pb5 ascaris suu
705	6	1.8	292	13	Q9YGM4	Q9ygm4 gallus gall	778	6	1.8	318	5	Q17090	Q17090 ascaris suu
706	6	1.8	293	3	Q94627	Q94627 schizosacch	779	6	1.8	318	5	Q95PB6	Q95pb6 ascaris suu
707	6	1.8	293	10	Q9AWY2	Q9awY2 oryza sativ	780	6	1.8	318	12	Q84147	Q84147 orf virus
708	6	1.8	293	16	P73482	P73482 synechocyst	781	6	1.8	318	15	Q98G95	Q98g95 rhizobium l
709	6	1.8	293	16	Q98D27	Q98d27 rhizobium l	782	6	1.8	319	10	Q9SX15	Q9sx15 chlamydomon
710	6	1.8	294	5	Q43946	Q43946 sarcocysts	783	6	1.8	319	10	Q9XHW4	Q9xhw4 oryza sativ
711	6	1.8	294	12	Q68225	Q68225 mouse cytom	784	6	1.8	319	17	Q26989	Q26989 methanoe
712	6	1.8	294	16	Q9CPI1	Q9cpi1 pasteurella	785	6	1.8	320	5	Q96620	Q96620 drosophila
713	6	1.8	294	17	Q9H1U7	Q9h1u7 thermoplas	786	6	1.8	320	5	Q9NAN9	Q9nan9 caenorhabdi
714	6	1.8	296	12	Q9DMEO	Q9dmeo rat cytoleg	787	6	1.8	320	5	Q9NAN9	Q9nan9 caenorhabdi
715	6	1.8	296	16	Q98KY0	Q98ky0 rhizobium l	788	6	1.8	320	16	Q58066	Q58066 pyrococcus
716	6	1.8	296	16	Q984Z4	Q984z4 rhizobium l	789	6	1.8	320	17	Q58066	Q58066 pyrococcus
717	6	1.8	297	2	Q9ETU9	Q9etu9 flavobacte	790	6	1.8	321	16	Q31154	Q31154 vibrio chol
718	6	1.8	297	11	Q9CYH3	Q9cyh3 mus musculu	791	6	1.8	321	16	Q9JX05	Q9jx05 neisseria m
719	6	1.8	298	16	Q98Q02	Q98q02 mycoplasma	792	6	1.8	321	16	Q9JX05	Q9jx05 neisseria m
720	6	1.8	299	4	Q13059	Q13059 homo sapien	793	6	1.8	321	16	Q9JX24	Q9jx24 neisseria m
721	6	1.8	299	10	Q9S056	Q9sq56 nicotiana t	794	6	1.8	321	16	Q9CF34	Q9cf34 lactococcus
722	6	1.8	299	10	Q9SVCI	Q9svci arabidopsis	795	6	1.8	322	5	Q9YCG0	Q9ycg0 aeropyrum p
723	6	1.8	299	16	Q9KCP0	Q9kcp0 bacillus ha	796	6	1.8	322	5	Q961V5	Q961v5 drosophila
724	6	1.8	299	17	Q27045	Q27045 mechanotner	797	6	1.8	322	16	Q9S7P1	Q9s7p1 oryza sativ
725	6	1.8	300	2	Q93F72	Q93f72 bacillus sp	798	6	1.8	323	5	Q9NKN7	Q9ncp9 pasteurella
726	6	1.8	300	2	Q93F70	Q93f70 bacillus sp	799	6	1.8	323	16	Q9CKC8	Q9ckc8 pasteurella
727	6	1.8	300	4	Q15868	Q15868 homo sapien	800	6	1.8	325	13	Q69501	Q69501 human herpe
728	6	1.8	300	5	Q9V4Q2	Q9v4q2 drosophila	801	6	1.8	325	13	Q90XK4	Q90xk4 pantodon bu
729	6	1.8	300	10	Q93979	Q93979 hyoscyamus	802	6	1.8	326	3	Q9HG15	Q9hgy5 candida alb
730	6	1.8	300	16	Q92982	Q929b2 listeria in	803	6	1.8	326	16	Q9AUI4	Q9aui4 medicago tr
731	6	1.8	301	16	Q9WZ55	Q9wz55 thermotoga	804	6	1.8	326	16	Q9CP26	Q9cp26 pasteurella
732	6	1.8	301	16	Q9RW36	Q9rw36 deinococcus	805	6	1.8	327	2	Q05083	Q05083 streptomyc
733	6	1.8	301	16	Q9K9T1	Q9k9t1 bacillus ha	806	6	1.8	327	17	Q9V2H9	Q9v2h9 pyrococcus
734	6	1.8	302	5	Q9GKX1	Q9gkx1 leishmania	807	6	1.8	328	4	Q96CA4	Q96ca4 homo sapien
735	6	1.8	302	10	Q40734	Q40734 oryza sativ	808	6	1.8	328	4	Q96CA4	Q96ca4 homo sapien
736	6	1.8	303	5	Q22981	Q22981 caenorhabdi	809	6	1.8	328	16	Q9KRN4	Q9krn4 vibrio chol
737	6	1.8	303	16	Q93566	Q93566 mycobacteri	810	6	1.8	328	16	Q9HY40	Q9hy40 pseudomonas
738	6	1.8	303	16	Q9HWL1	Q9hw1 pseudomonas	811	6	1.8	329	5	Q9HY08	Q9hy08 pseudomonas
739	6	1.8	304	2	Q9ALP7	Q9alp7 bordetella	812	6	1.8	329	13	Q91AV6	Q91av6 spheroides
740	6	1.8	305	2	Q9L259	Q9l259 streptomyc	813	6	1.8	329	16	Q93017	Q93017 bacillus su
741	6	1.8	305	3	Q94417	Q94417 schizosacch	814	6	1.8	330	10	Q944B9	Q944b9 sambucus ni
742	6	1.8	305	4	Q9H9S0	Q9h9s0 homo sapien	815	6	1.8	330	11	P97269	P97269 cavia porce
743	6	1.8	305	10	Q9ZWC1	Q9zwc1 arabidopsis	816	6	1.8	330	16	Q92X30	Q92x30 rhizobium m
744	6	1.8	306	5	Q95SR5	Q95sr5 drosophila	817	6	1.8	330	15	Q92T17	Q92t17 rhizobium m
745	6	1.8	306	16	Q98GP2	Q98gp2 rhizobium l	818	6	1.8	331	5	Q17151	Q17151 caenorhabdi
746	6	1.8	306	16	Q98BMO	Q98bmo rhizobium l	819	6	1.8	332	4	Q60530	Q60530 homo sapien

820	6	1.8	332	4	09H5L4	09h5l4 homo sapien	893	6	1.8	355	2	046402	046402 chlamydia t
821	6	1.8	333	4	09Bv77	09bv77 homo sapien	894	6	1.8	355	3	005881	005881 saccharomyc
822	6	1.8	333	4	045419	045419 caenorhabd1	895	6	1.8	355	5	0961C4	0961C4 drosophila
823	6	1.8	333	8	09T9H2	09t9h2 halocynthia	896	6	1.8	355	7	030766	030766 macropus ru
824	6	1.8	333	10	09ZT61	09zt61 sambucus ni	897	6	1.8	355	16	09A7H8	09a7h8 caulobacter
825	6	1.8	333	10	09ZT60	09zt60 sambucus ni	898	6	1.8	356	2	069155	069155 streptococc
826	6	1.8	333	10	09SY54	09sy54 sambucus ni	899	6	1.8	356	5	09S5M5	09s5m5 drosophila
827	6	1.8	333	10	09SY55	09sy55 sambucus ni	900	6	1.8	356	16	099ZK3	099zk3 streptococc
828	6	1.8	334	5	09V1S3	09v1s3 drosophila	901	6	1.8	356	16	0970P2	097p2 streptococc
829	6	1.8	334	16	09KGG5	09kgs5 bacillus ha	902	6	1.8	357	2	09L4N5	09l4n5 lactococcus
830	6	1.8	334	17	057833	057833 pyrococcus	903	6	1.8	357	16	09CHR2	09chr2 lactococcus
831	6	1.8	335	2	093RM6	093rm6 streptomyce	904	6	1.8	357	16	09CFB0	09cfb0 lactococcus
832	6	1.8	335	5	09N6L3	09n6l3 caenorhabd1	905	6	1.8	358	10	09S7S1	09s7s1 arabidopsis
833	6	1.8	335	5	09NF70	09nf70 caenorhabd1	906	6	1.8	360	16	09A0C7	09a0c7 streptococc
834	6	1.8	335	5	09NF69	09nf69 caenorhabd1	907	6	1.8	361	10	09F1X4	09f1x4 arabidopsis
835	6	1.8	335	16	09HMY7	09hmy7 pseudomonas	908	6	1.8	361	16	09BM55	09bm55 rhizobium l
836	6	1.8	335	16	099WY9	099wy9 staphylococ	909	6	1.8	362	10	09FFW9	09ffw9 arabidopsis
837	6	1.8	336	2	069606	069606 moraxella s	910	6	1.8	363	5	09VB82	09vb82 drosophila
838	6	1.8	336	5	021716	021716 caenorhabd1	911	6	1.8	363	10	09M377	09m377 arabidopsis
839	6	1.8	336	10	0944B8	0944b8 sambucus ni	912	6	1.8	363	17	059026	059026 pyrococcus
840	6	1.8	336	13	09YHWS	09yhw5 gallus gall	913	6	1.8	363	17	09V0D3	09v0d3 pyrococcus
841	6	1.8	336	16	092VM9	092vm9 rhizobium m	914	6	1.8	364	2	09RDP0	09rdp0 streptomyce
842	6	1.8	337	4	09Y2S5	09y2s5 homo sapien	915	6	1.8	364	16	09BCR3	09bc3 rhizobium l
843	6	1.8	337	4	096C86	096c86 homo sapien	916	6	1.8	365	4	09H3E0	09h3e0 homo sapien
844	6	1.8	337	11	09CZM2	09czm2 mus musculu	917	6	1.8	365	16	09RHH9	09rhh9 delnoccocus
845	6	1.8	337	11	P97268	P97268 cavia porce	918	6	1.8	366	2	09Z504	09z504 streptomyce
846	6	1.8	337	16	09PEG4	09peg4 xyella fas	919	6	1.8	366	5	09SPB4	09spb4 ascaris suu
847	6	1.8	337	17	0971J2	0971j2 sulfolobus	920	6	1.8	366	10	004592	004592 arabidopsis
848	6	1.8	338	11	09PAR7	09par7 mus musculu	921	6	1.8	366	17	097AP5	097ap5 thermoplasm
849	6	1.8	338	16	09AAU4	09aa4 caulobacter	922	6	1.8	367	10	09EXT5	09ext5 oryza sativ
850	6	1.8	338	16	09BH37	09bh37 rhizobium l	923	6	1.8	367	10	09M166	09m166 arabidopsis
851	6	1.8	339	4	099772	099772 homo sapien	924	6	1.8	367	13	091905	091905 xenopus lae
852	6	1.8	339	5	021788	021788 caenorhabd1	925	6	1.8	369	8	098998	098998 vigna radia
853	6	1.8	339	11	070530	070530 mus musculu	926	6	1.8	370	5	096081	096081 neurospora
854	6	1.8	339	11	09D4F8	09d4f8 mus musculu	927	6	1.8	370	5	095017	095017 drosophila
855	6	1.8	340	2	09KHK3	09khk3 streptomyce	928	6	1.8	370	13	091904	091904 xenopus lae
856	6	1.8	340	2	09EMX3	09emx3 streptomyce	929	6	1.8	370	13	057675	057675 xenopus lae
857	6	1.8	341	16	09PEV1	09pev1 xyella fas	930	6	1.8	371	5	046052	046052 drosophila
858	6	1.8	341	16	099WM7	099wm7 staphylococ	931	6	1.8	372	4	060529	060529 homo sapien
859	6	1.8	341	16	092CU9	092cu9 listeria in	932	6	1.8	372	11	09CXT1	09cxt1 mus musculu
860	6	1.8	342	4	09BVR6	09bvr6 homo sapien	933	6	1.8	372	16	P95018	P95018 mycobacteri
861	6	1.8	343	10	022826	022826 arabidopsis	934	6	1.8	373	4	096ML3	096ml3 homo sapien
862	6	1.8	343	16	098602	098602 rhizobium l	935	6	1.8	373	8	09MU96	09mu96 ungaria fio
863	6	1.8	344	8	094V75	094v75 lanthanotus	936	6	1.8	373	16	092M05	092m05 rhizobium m
864	6	1.8	344	13	09PESJ1	09pesj1 ictalurus p	937	6	1.8	374	10	09M2R9	09m2r9 arabidopsis
865	6	1.8	344	13	096SH0	096sh0 ictalurus p	938	6	1.8	374	16	09PKY2	09pk2 chlamydia m
866	6	1.8	344	16	034829	034829 bacillus su	939	6	1.8	375	2	066290	066290 agrobacteri
867	6	1.8	345	5	09Y161	09y161 drosophila	940	6	1.8	375	17	0978J3	0978j3 thermoplasm
868	6	1.8	345	5	09XUR5	09xur5 caenorhabd1	941	6	1.8	376	2	09Z6F5	09z6f5 vibrio para
869	6	1.8	345	10	09LS32	09ls32 physcomitre	942	6	1.8	376	2	09R6T6	09r6t6 bacteroides
870	6	1.8	345	11	09D790	09d790 mus musculu	943	6	1.8	376	6	09SKT0	09skt0 macaca fasc
871	6	1.8	346	2	087156	087156 vibrio chol	944	6	1.8	376	8	0957A9	0957a9 myotis levi
872	6	1.8	346	5	09W368	09w368 drosophila	945	6	1.8	376	8	0956Z7	0956z7 myotis oxvo
873	6	1.8	346	16	09RVT6	09rvt6 delnoccocus	946	6	1.8	376	16	09CCS1	09ccs1 mycobacteri
874	6	1.8	346	16	09KAS5	09kas5 bacillus ha	947	6	1.8	377	10	09PMU1	09pmu1 oryza sativ
875	6	1.8	347	2	09S0N9	09s0n9 streptomyce	948	6	1.8	377	16	09PE47	09pe47 xyella fas
876	6	1.8	347	4	09ALP5	09alp5 bordetella	949	6	1.8	378	16	066423	066423 mycobacteri
877	6	1.8	347	4	09NML4	09nml4 homo sapien	950	6	1.8	378	17	0976U8	0976u8 sulfolobus
878	6	1.8	348	16	09CLB2	09clb2 pasteurella	951	6	1.8	379	5	020936	020936 caenorhabd1
879	6	1.8	348	4	096GZ7	096gz7 homo sapien	952	6	1.8	379	8	0957A8	0957a8 myotis luci
880	6	1.8	348	5	09XAH6	09xah6 caenorhabd1	953	6	1.8	379	8	0956Z8	0956z8 myotis nigr
881	6	1.8	348	5	09TXJ0	09txj0 caenorhabd1	954	6	1.8	379	8	0956Z1	0956z1 myotis vola
882	6	1.8	348	12	09S3U2	09s3u2 o'nyong-nyo	955	6	1.8	379	8	0956Z0	0956z0 myotis vola
883	6	1.8	348	12	09J5U1	09j5u1 o'nyong-nyo	956	6	1.8	380	10	033751	033751 arabcia lix
884	6	1.8	349	2	056775	056775 xanthomonas	957	6	1.8	380	10	081721	081721 arabidopsis
885	6	1.8	351	4	09C0F9	09c0f9 homo sapien	958	6	1.8	380	16	09KT24	09kt24 vibrio chol
886	6	1.8	352	16	0914W9	0914w9 pseudomonas	959	6	1.8	381	4	09Y408	09y408 homo sapien
887	6	1.8	353	5	09VLL7	09vll7 drosophila	960	6	1.8	381	5	020503	020503 caenorhabd1
888	6	1.8	353	13	09YHJ3	09yhj3 lampetra fl	961	6	1.8	381	10	09LDD5	09ldz5 arabidopsis
889	6	1.8	353	16	092ZP8	092zp8 rhizobium m	962	6	1.8	382	5	09VV92	09vv92 drosophila
890	6	1.8	354	2	09XA39	09xa39 streptomyce	963	6	1.8	382	5	027438	027438 amlyomma a
891	6	1.8	354	4	015867	015867 homo sapien	964	6	1.8	383	8	094Y26	094y26 psylliella l
892	6	1.8	354	16	0915Y7	0915y7 pseudomonas	965	6	1.8	383	16	025795	025795 helicobacte

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966 6 1.8 383 16 092K33 092K33 helicobacte
967 6 1.8 384 16 09N441 09N441 caenorhabdi
968 6 1.8 384 16 09A7D1 09A7D1 caulobacter
969 6 1.8 385 10 09C6K4 09C6K4 arabidopsis
970 6 1.8 385 16 099TE1 099TE1 staphylococ
971 6 1.8 386 16 09A5M7 09A5M7 caulobacter
972 6 1.8 387 2 09ZT11 09ZT11 streptococ
973 6 1.8 387 16 09K675 09K675 bacillus ha
974 6 1.8 388 2 054466 054466 streptomyce
975 6 1.8 388 4 096C95 096C95 homo sapien
976 6 1.8 388 16 09KNP8 09KNP8 vibrio chol
977 6 1.8 389 2 094200 094200 azotobacter
978 6 1.8 389 11 091ZV3 091ZV3 cavia porce
979 6 1.8 389 11 090WN1 090WN1 xenopus lae
980 6 1.8 389 16 09HWY6 09HWY6 pseudomonas
981 6 1.8 390 2 095540 095540 pediococcus
982 6 1.8 390 2 050279 050279 pseudomonas
983 6 1.8 390 2 093DB5 093DB5 agrobacteri
984 6 1.8 390 6 09GKX0 09GKX0 macaca fasc
985 6 1.8 390 10 091XG5 091XG5 arabidopsis
986 6 1.8 391 2 091324 091324 pseudomonas
987 6 1.8 391 2 09X684 09X684 pseudomonas
988 6 1.8 391 2 09X685 09X685 pseudomonas
989 6 1.8 391 2 086769 086769 streptomyce
990 6 1.8 391 2 095475 095475 pseudomonas
991 6 1.8 391 5 09YUJ5 09YUJ5 drosophila
992 6 1.8 391 11 09ESS9 09ESS9 rattus norv
993 6 1.8 391 11 091WR9 091WR9 mus musculu
994 6 1.8 391 16 098IM6 098IM6 rhizobium l
995 6 1.8 392 2 030529 030529 pseudomonas
996 6 1.8 392 2 030529 030529 pseudomonas
997 6 1.8 392 2 09RLI7 09RLI7 streptomyce
998 6 1.8 392 16 09CE08 09CE08 lactococcus
999 6 1.8 393 2 091A23 091A23 streptococ
1000 6 1.8 393 2 09RNH2 09RNH2 rhodospir
092WC3 rhizobium m

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ALIGNMENTS

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RESULT 1
ID 020468 PRELIMINARY; PRT; 137 AA.
AC 020468;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE F46F2.3 PROTEIN.
GN F46F2.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN 01
RP SEQUENCE FROM N.A.
RA Thomas K.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RT none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z69903; CA93772.1; -.
SO SEQUENCE 137 AA; 14265 MW; 46CBDD4ABE352114 CRC64;

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Query Match 2.7%; Score 9; DB 5; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 126 QQPAYQPOP 134

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Db 67 QQPAYQPOP 75
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RESULT 2
ID 09WLL1 PRELIMINARY; PRT; 522 AA.
AC 09WLL1;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GAG PROTEIN.
GN GAG.
OS Mus dunnii endogenous virus.
OC Viruses; Retroid viruses; Retroviridae; Gammaetrovirus.
OX NCBI_TaxID=75986;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=98362151; PubMed=9696842;
RA Wolgamot G., Bonham L., Miller A.D.;
RT "Sequence analysis of Mus dunnii endogenous virus reveals a hybrid
RT VL30/Gibbon ape leukemia virus-like structure and a distinct
RT envelope."
RL J. Virol. 72:7459-7466(1998).
RN 12
RP SEQUENCE FROM N.A.
RA Wolgamot G., Bonham L., Miller A.D.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF053745; AAC31804.1; -.
DR InterPro: IPR000840; GAG_MA.
DR InterPro: IPR003036; GAG_P30.
DR InterPro: IPR01878; Zn1_CCHC.
DR Pfam: PF01140; GAG_MA; 1.
DR Pfam: PF02093; GAG_P30; 1.
DR Pfam: PF00098; zf-CCHC; 1.
DR SMART: SM00343; ZnF_C2HC; 1.
KW Core protein; Polyprotein; Zinc-finger.
SQ SEQUENCE 522 AA; 58597 MW; 0E7A04D319698B1C CRC64;

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Query Match 2.7%; Score 9; DB 15; Length 522;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 169 PVAAPQPOP 177
|||||||
Db 156 PVAAPQPOP 164
RESULT 3
ID 089814 PRELIMINARY; PRT; 622 AA.
AC 089814;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GLYCOSYLATED GAG PROTEIN.
GN GAG.
OS Mus dunnii endogenous virus.
OC Viruses; Retroid viruses; Retroviridae; Gammaetrovirus.
OX NCBI_TaxID=75986;
RN 11
RP SEQUENCE FROM N.A.
RX MEDLINE=98362151; PubMed=9696842;
RA Wolgamot G., Bonham L., Miller A.D.;
RT "Sequence analysis of Mus dunnii endogenous virus reveals a hybrid
RT VL30/Gibbon ape leukemia virus-like structure and a distinct
RT envelope."
RL J. Virol. 72:7459-7466(1998).
RN 12
RP SEQUENCE FROM N.A.
RA Wolgamot G., Bonham L., Miller A.D.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

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DR EMBL: AF053745; AAC31803.1; -
DR InterPro: IPR000840; Gag_MA.
DR InterPro: IPR003036; Gag_P30.
DR InterPro: IPR001878; Znf_CCHC.
DR Pfam: PF01140; gag_MA.1.
DR Pfam: PF02093; Gag_P30.1.
DR Pfam: PF00098; zfc_CCHC.1.
DR SMART: SM00343; Znf_C2HC.1.
KW Core protein; Polyprotein; Zinc-finger.
SQ SEQUENCE 622 AA; 69125 MW; 159BCFB052106CD3 CRC64;

Query Match 2.4%; Score 8; DB 15; Length 622;
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 PVAAPQEP 177
|||||||
DB 256 PVAAPQEP 264

RESULT 4
O9HNM8 PRELIMINARY; PRT; 130 AA.
AC O9HNM8;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)
DE VNG2029H.
GN VNG2029H.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
OC Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahalas G.G., Bergquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Bailas N.S., Thorsson V., Shroana J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Weir R., Geo Y.A.,
RA Leitbauer B., Keller K., Cruz R., Danon M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angerine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hod L., Dassarma S.;
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL: AE005096; AAG20192.1; -
KW Complete proteome.
SQ SEQUENCE 130 AA; 12950 MW; 91FE13451FD59892 CRC64;

Query Match 2.4%; Score 8; DB 17; Length 130;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 166 PAEVPAAP 173
|||||||
DB 74 PAEVPAAP 81

RESULT 5
O9XYB2 PRELIMINARY; PRT; 210 AA.
AC O9XYB2;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE MERZOITRE SURFACE PROTEIN 4/5.
GN MSP4/5.
OS Plasmodium chabaudi adam.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5826;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DS;
RX MEDLINE=99242782; PubMed=10225857;
RA Black C.G., Wang L., Hibbs A.R., Werner E., Coppel R.L.;
RT "Identification of the Plasmodium chabaudi homologue of merozoite
surface proteins 4 and 5 of Plasmodium falciparum."
RL Infect. Immun. 67:2075-2081(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-DS;
RX MEDLINE=20078867; PubMed=10613706;
RA Kedzierski L., Black C.G., Coppel R.L.;
RT "Characterization of the merozoite surface protein 4/5 gene of
Plasmodium berghei and Plasmodium yoelii."
RL Mol. Biochem. Parasitol. 105:137-147(2000).
DR EMBL: AF080446; AAD28328.1; -
DR InterPro: IPR000561; EGF-like.
DR SMART: SM00181; EGF.1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
SQ SEQUENCE 210 AA; 22279 MW; 49364FE8EA2ACD42 CRC64;

Query Match 2.4%; Score 8; DB 5; Length 210;
Best Local Similarity 100.0%; Pred. No. 8.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 AIAIALL 21
|||||||
DB 202 AIAIALL 209

RESULT 6
O9ADC6 PRELIMINARY; PRT; 222 AA.
ID O9ADC6;
AC O9ADC6;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE SPDA2 PROTEIN.
GN SPDA2.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Saunders D.C., Harris D.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RA Cerdano A.M., Parhill J., Barrell B.G., Rajandream M.A.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-A3(2);
RX MEDLINE=97000351; PubMed=8843436;
RA Redenbach M., Kleser H.M., Denapate D., Eichner A., Cullum J.,
RA Kinashi H., Hopwood D.A.;
RT "A set of ordered cosmids and a detailed genetic and physical map for
the 8 Mb Streptomyces coelicolor A3(2) chromosome."
RL Mol. Microbiol. 21:77-96(1996).
DR EMBL: AL589707; CAC33905.1; -
SQ SEQUENCE 222 AA; 23251 MW; B74F3719B4BF310A CRC64;

Query Match 2.4%; Score 8; DB 2; Length 222;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 177 PVAEPAPV 184

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Db      159 PVAEPAV 166
|||||||
RESULT 7
ID      092LX9      PRELIMINARY;      PRT;      234 AA.
AC      092LX9:
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      HYPOTHETICAL TRANSMEMBRANE PROTEIN SMC03152.
GN      SMC03152.
OS      Rhizobium meliloti (Sinorhizobium meliloti).
OC      Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC      Rhizobiaceae; Sinorhizobium.
OX      NCBI_TaxID=382;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=1021;
RX      MEDLINE=21368234; PubMed=11474104;
RA      Gallibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F.,
RA      Barloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G.,
RA      Bouty M., Bowser L., Buhrmester J., Cadieu N.A., Capela D., Chain P.,
RA      Cowie A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F.,
RA      Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M.,
RA      Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D.,
RA      Kahn M.L., Kallman S., Keating D.H., Kiss E., Komp C., Lelaure V.,
RA      Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Lelaure V.,
RA      Ramsberger U., Surzycki R., Thebaud P., Vandenoel M.,
RA      Vorholter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J.;
RT      "The composite genome of the legume symbiont Sinorhizobium meliloti."
RL      Science 293:668-672(2001).
DR      EMBL: AL591792; CAC47462.1;
KW      Hypothetical protein; Complete proteome.
SQ      SEQUENCE 234 AA; 23951 MW; 441A80844492F44 CRC64;

Query Match      2.4%; Score 8; DB 16; Length 234;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      176 EPVAEPAP 183
|||||||
Db      86 EPVAEPAP 93

RESULT 8
ID      095RV8      PRELIMINARY;      PRT;      400 AA.
AC      095RV8:
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      LD03043P.
GN      ACPL.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=Y, CN BW SP;
RA      Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA      Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA      Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA      Nuno J., Pacleb J., Paragas V., Park S., Pionuamvong S., Wan K.,
RA      Yu C., Lewis S.E., Rubin G.M., Celisner S.;
RL      Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AY061103; AAL28651.1;
SQ      SEQUENCE 400 AA; 46108 MW; 84BFE4E8F8FFDC5D CRC64;

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Query Match      2.4%; Score 8; DB 5; Length 400;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      54 DEVEDDE 61
|||||||
Db      93 DEVEDDE 100

RESULT 9
ID      09S333      PRELIMINARY;      PRT;      431 AA.
AC      09S333:
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      HYPOTHETICAL 46.3 KDA PROTEIN.
GN      ORF431.
OS      Prochlorococcus marinus.
OC      Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC      Prochlorococcus.
OX      NCBI_TaxID=1219;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CCMP 1375;
RX      MEDLINE=97008144; PubMed=8855320;
RA      Hess W.R., Partensky F., van der Staay G.W., Garcia-Fernandez J.M.,
RA      Boerner T., Vaulot D.;
RT      "Coexistence of phycoerythrin and a chlorophyll a/b antenna in a
RT      marine prokaryote."
RL      Proc. Natl. Acad. Sci. U.S.A. 93:11126-11130(1996).
DR      [2]
KW      SEQUENCE FROM N.A.
RP      STRAIN=CCMP 1375;
RX      MEDLINE=99364545; PubMed=10437834;
RA      Hess W.R., Steglich C., Lichtle C., Partensky F.;
RT      "Phycocyanins of the oxyphotobacterium Prochlorococcus marinus are
RT      associated to the thylakoid membrane and are encoded by a single large
RT      gene cluster."
DR      Plant Mol. Biol. 40:507-521(1999).
DR      EMBL: AJ001230; CAB52700.1;
KW      Hypothetical protein.
SQ      SEQUENCE 431 AA; 46291 MW; B2D73641FA95F729 CRC64;

Query Match      2.4%; Score 8; DB 2; Length 431;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 IIVGAIAI 17
|||||||
Db      138 IIVGAIAI 145

RESULT 10
ID      057311      PRELIMINARY;      PRT;      441 AA.
AC      057311:
DT      01-JUN-1998 (TREMBLrel. 06, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE      01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE      ZINC FINGER PROTEIN ZIC 3 (ZINC FINGER PROTEIN OF THE CEREBELLUM 3)
DE      (ZIC3 PROTEIN).
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      MEDLINE=98004509; PubMed=9342348;
RA      Nakata K., Nagai T., Aruga J., Mikoshiba K.;

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RT Xenopus zic3, a primary regulator both in neural and neural crest development.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:11980-11985(1997).
 RN [12]
 RP REVISIONS.
 RA Nakata K., Nagai T., Aruga J., Mikoshiba K.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CAN DETERMINE THE ECTODERMAL CELL FATE AND PROMOTE THE EARLIEST STEP OF NEURAL AND NEURAL CREST DEVELOPMENT.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- TISSUE SPECIFICITY: CNS. A HIGH LEVEL EXPRESSION IS SEEN IN THE CEREBELLUM.
 CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED AT EARLY GASTRULA IN DORSAL LIP AND PROSPECTIVE NEURAL PLATE. IT THEN DECREASED IN THE DORSAL LIP AND INCREASED IN THE PROSPECTIVE NEURAL PLATE. AT THE NEURAL PLATE STAGE, IT IS EXPRESSED STRONGLY IN PROSPECTIVE REGION OF MESENCEPHALON AND ANTERIOR RHOMBENCEPHALON. AT EARLY TAILBUD STAGES, IT BECAME RESTRICTED TO THE DORSAL REGION OF FOREBRAIN, MIDBRAIN, AND HINDBRAIN, AND WEAKLY TO THE DORSAL REGION OF THE TRUNK. AFTER MID-TAILBUD STAGE, IT DECREASED IN THE DIENCEPHALON, APPEARED IN THE LATERAL MESODERM OF THE TAILBUD REGION AND IS RESTRICTED IN THE DORSAL PART OF THE NEURAL TUBE.
 CC -1- SIMILARITY: TO THE GLI-RELATED GROUP OF C2H2-TYPE ZINC-FINGERS PROTEINS.
 CC EMBL: AB005292; BAA23874.2; -.
 CC HSSP: P08047; ISP2.
 DR InterPro: IPR000822; znf-C2H2.
 DR Pfam: PF00096; znf-C2H2; 5.
 DR SMART: SM00355; znf-C2H2; 5.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 3.
 DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 4.
 KW Developmental protein; Neurogenesis; Zinc-finger; Metal-binding;
 KM DNA-binding; Repeat; Nuclear protein; Multigene family.
 FT ZN_FING 222 257 C2H2-TYPE (ATYPICAL).
 FT ZN_FING 266 293 C2H2-TYPE
 FT ZN_FING 299 323 C2H2-TYPE (ATYPICAL).
 FT ZN_FING 329 353 C2H2-TYPE
 FT ZN_FING 359 381 C2H2-TYPE
 SQ SEQUENCE 441 AA; 48481 MW; FB8F340A2E3EDA4E CRC64;
 Query Match 2.4%; Score 8; DB 13; Length 441;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 197 MNVAHHG 204
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 Db 199 MNVAHHG 206
 RESULT 11
 Q9SSF3 PRELIMINARY; PRT; 457 AA.
 AC Q9SSF3;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE MLP3.2 PROTEIN.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA.
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
 RA Rongling C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome III PL MLP3 genomic sequence.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC009176; AF13075.1; -.

SQ SEQUENCE 457 AA; 50356 MW; 03564C83112632CA CRC64;
 Query Match 2.4%; Score 8; DB 10; Length 457;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 ILITVCAI 15
 |||||
 Db 223 ILITVCAI 230
 RESULT 12
 ID Q9CGA7 PRELIMINARY; PRT; 512 AA.
 AC Q9CGA7;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-OCT-2001 (Tremblrel. 18, Last annotation update)
 DE CITRATE LYASE ALPHA CHAIN (EC 4.1.3.6).
 GN CITF.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 CC Lactococcus.
 OX NCBI_TaxID=1360;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=11337471;
 RA Bolotin A., Winkler P., Mauer S., Jallion O., Malarne K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403.";
 RL Genome Res. 11:731-753(2001).
 DR EMBL: AE006351; AAK05289.1; -.
 KW Lyase; Complete proteome.
 SQ SEQUENCE 512 AA; 55440 MW; AF6851813614C0C4 CRC64;
 Query Match 2.4%; Score 8; DB 16; Length 512;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 318 DIIEVVD 325
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 Db 505 DIIEVVD 512
 RESULT 13
 ID Q9VKLO PRELIMINARY; PRT; 620 AA.
 AC Q9VKLO;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE CG14917 PROTEIN.
 GN SAMUEL OR CG1291 OR CG14917 OR CG14918.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscormorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY.
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abtill J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Botchan M.R., Bouck J., Brckstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarly C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relneer K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003630; MAF53057.1; -
 DR FlyBase: FBgn0123350; Samuel.
 SQ SEQUENCE 620 AA; 62463 MW; DFD8BA827FFD385D CRC64;

Query Match 2.4% Score 8; DB 5; Length 620;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 101 LNS100A 108
 Oy 212 LNS100A 219
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 Db 101 LNS100A 108
 RESULT 14
 09Y0W1 PRELIMINARY; PRT; 1476 AA.
 AC 09Y0W1;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE ATP-DEPENDENT CHROMATIN ASSEMBLY FACTOR LARGE SUBUNIT.
 GN ACF1 OR CG1966.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_Taxid=7227;
 ON [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99315627; PubMed=10385622;
 RA Ito T., Levenstein M.E., Eyodorov D.V., Kutach A.K., Kobayashi R.,
 RA Kadohaga J.T.;
 RT ACF consists of two subunits, Acf1 and ISW1, that function
 RT cooperatively in the ATP-dependent catalysis of chromatin assembly.";
 RL Genes Dev. 13:1529-1539(1999).
 DR EMBL: AF148963; AAD38952.1; -
 DR FlyBase: FBgn0027620; Acf1.
 DR InterPro: IPR001487; Bromodomain.
 DR InterPro: IPR001064; Crystallin.
 DR InterPro: IPR004022; DDT.
 DR InterPro: IPR001965; PHD.

DR Pfam: PF00439; bromodomain; 1.
 DR Pfam: PF00628; PHD; 2.
 DR PRINTS: PR00503; BROMODOMAIN.
 DR SMART: SM00297; BROMO; 1.
 DR SMART: SM00249; PHD; 2.
 DR PROSITE: PSS0014; BROMODOMAIN_2; 1.
 DR PROSITE: PSS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 DR PROSITE: PSS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
 SQ SEQUENCE 1476 AA; 170457 MW; C18A6CEBF57E6B3 CRC64;
 Query Match 2.4% Score 8; DB 5; Length 1476;
 Best Local Similarity 100.0%; Pred. No. 49;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1169 DEVEDDE 1176
 Oy 54 DEVEDDE 61
 |||||
 Db 1169 DEVEDDE 1176
 RESULT 15
 09Y9T4 PRELIMINARY; PRT; 1476 AA.
 AC 09Y9T4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE ACF1 PROTEIN.
 GN ACF1 OR CG1966.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_Taxid=7227;
 ON [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Cealiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mikos D.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Balieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Botchan M.R., Bouck J., Brckstein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarly C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relneer K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003779; AAF57200.1; -.
DR FlyBase: FBgn027620; Acfl.
DR InterPro: IPR001487; Bromodomain.
DR InterPro: IPR001064; Crystallin.
DR InterPro: IPR004022; DDT.
DR InterPro: IPR001965; PHD.
DR Pfam: PF00439; bromodomain; 1.
DR Pfam: PF00628; PHD; 2.
DR PRINTS: PR00503; BROMODOMAIN.
DR SMART: SM00297; BROMO; 1.
DR SMART: SM00249; PHD; 2.
DR PROSITE: PSS0014; BROMODOMAIN_2; 1.
DR PROSITE: PSS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SQ SEQUENCE 1476 AA; 170410 MW; 9EE1906672E5B006 CRC64;

Query Match 2.48; Score 8; DB 5; Length 1476;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 DEDVEDDE 61
| | | | | | | |
DB 1169 DEDVEDDE 1176

Search completed: September 25, 2002, 09:56:57
Job time: 256 sec

